

	BRACE2007518//	0	//	0.000	//	2.707
	BRACE2007798//	0	//	0.000	//	1.234
	BRACE2008653//	0	//	0.000	//	4.403
	BRACE2008941//	0	//	0.000	//	11.920
5	BRACE2009037//	0	//	0.000	//	0.697
	BRACE2009517//	0	//	0.000	//	6.470
	BRACE2011183//	0	//	0.000	//	7.667
	BRACE2012528//	0	//	0.000	//	0.566
	BRACE2017397//	0	//	0.000	//	11.252
10	BRACE2017574//	0	//	0.000	//	6.110
	BRACE2019147//	0	//	0.000	//	2.554
	BRACE2020584//	0	//	0.000	//	62.692
	BRACE2022333//	0	//	0.000	//	10.589
	BRACE2022638//	0	//	0.000	//	2.667
15	BRACE2027896//	0	//	0.000	//	30.503
	BRACE2030341//	0	//	0.000	//	16.499
	BRACE2037310//	0	//	0.000	//	23.401
	BRACE2045445//	0	//	0.000	//	62.692
	BRACE3004371//	0	//	0.000	//	4.481
20	BRACE3005938//	0	//	0.000	//	1.313
	BRACE3007258//	0	//	0.000	//	15.521
	BRACE3008772//	0	//	0.000	//	62.692
	BRACE3010428//	0	//	0.000	//	5.461
	BRACE3027478//	0	//	0.000	//	19.089
25	BRACE3040863//	0	//	0.000	//	21.335
	BRALZ2009446//	0	//	0.000	//	5.561
	BRALZ2009482//	0	//	0.000	//	0.443
	BRALZ2017359//	0	//	0.000	//	24.816
	BRAMY2000585//	0	//	0.000	//	2.929
30	BRAMY2004363//	0	//	0.000	//	12.191
	BRAMY2004521//	0	//	0.000	//	5.654
	BRAMY2006366//	0	//	0.000	//	10.987
	BRAMY2009123//	0	//	0.000	//	54.206
	BRAMY2009934//	0	//	0.000	//	7.051
35	BRAMY2011105//	67.510	//	0	//	0.000
	BRAMY2012536//	0	//	0.000	//	0.688

	BRAMY2013659//	0	//	0.000	//	34.645
	BRAMY2019989//	0	//	0.000	//	1.150
	BRAMY2020427//	0	//	0.000	//	0.706
	BRAMY2022168//	0	//	0.000	//	16.134
5	BRAMY2026685//	0	//	0.000	//	2.956
	BRAMY2028740//	0	//	0.000	//	1.110
	BRAMY2031516//	0	//	0.000	//	8.809
	BRAMY2032087//	0	//	0.000	//	4.333
	BRAMY2040095//	0	//	0.000	//	0.815
10	BRAMY3002458//	0	//	0.000	//	14.807
	BRAMY3005184//	0	//	0.000	//	26.725
	BRAWH1000040//	0	//	0.000	//	2.462
	BRAWH1000093//	10.279	//	0	//	2.200
	BRAWH2000082//	0	//	0.000	//	0.457
15	BRAWH2000488//	0	//	0.000	//	12.025
	BRAWH2000588//	0	//	0.000	//	1.496
	BRAWH2000633//	0	//	0.000	//	1.581
	BRAWH2000697//	0	//	0.000	//	1.206
	BRAWH2000839//	0	//	0.000	//	0.980
20	BRAWH2001092//	0	//	0.000	//	1.677
	BRAWH2001141//	0	//	0.000	//	6.061
	BRAWH2001412//	0	//	0.000	//	17.933
	BRAWH2001439//	0	//	0.000	//	1.227
	BRAWH2002601//	0	//	0.000	//	5.932
25	BRAWH2003693//	0	//	0.000	//	4.080
	BRAWH2004078//	0	//	0.000	//	6.285
	BRAWH2005578//	0	//	0.000	//	15.983
	BRAWH2005661//	0	//	0.000	//	1.907
	BRAWH2007605//	0	//	0.000	//	2.446
30	BRAWH2008058//	0	//	0.000	//	27.939
	BRAWH2009238//	0	//	0.000	//	6.217
	BRAWH2011343//	0	//	0.000	//	8.367
	BRAWH2012698//	0	//	0.000	//	22.868
	BRAWH2014188//	0	//	0.000	//	11.100
35	BRAWH2014473//	0	//	0.000	//	54.394
	BRAWH2014645//	0	//	0.000	//	2.522

	BRAWH2016166//	0	//	0.000	//	18.040
	BRAWH2017304//	0	//	0.000	//	19.804
	BRAWH2017685//	0	//	0.000	//	1.211
	BRAWH2018526//	0	//	0.000	//	0.367
5	BRAWH2018745//	0	//	0.000	//	54.394
	BRAWH3000314//	0	//	0.000	//	28.447
	BRAWH3001326//	0	//	0.000	//	54.394
	BRAWH3002574//	0	//	0.000	//	7.885
	BRAWH3002853//	0	//	0.000	//	1.764
10	BRAWH3003727//	0	//	0.000	//	11.993
	BRAWH3004350//	0	//	0.000	//	19.774
	BRAWH3016271//	0	//	0.000	//	6.433
	BRAWH3021545//	0	//	0.000	//	17.404
	BRAWH3026529//	0	//	0.000	//	54.394
15	BRAWH3029806//	0	//	0.000	//	10.629
	BRCAN2003944//	0	//	0.000	//	0.336
	BRCAN2009432//	29.345	//	0	//	3.141
	BRCAN2011946//	0	//	0.000	//	7.542
	BRCAN2021024//	0	//	0.000	//	24.461
20	BRCAN2022126//	0	//	0.000	//	5.791
	BRCAN2024572//	0	//	0.000	//	3.257
	BRCAN2028355//	0	//	0.000	//	1.762
	BRCOC1000040//	0	//	0.000	//	14.069
	BRCOC2000333//	0	//	0.000	//	14.286
25	BRCOC2003187//	0	//	0.000	//	0.938
	BRCOC2010730//	0	//	0.000	//	12.892
	BRCOC2012172//	0	//	0.000	//	6.710
	BRCOC2012551//	0	//	0.000	//	8.602
	BRCOC2015597//	0	//	0.000	//	25.187
30	BRHIP2001099//	0	//	0.000	//	8.268
	BRHIP2003062//	0	//	0.000	//	56.647
	BRHIP2007305//	0	//	0.000	//	1.350
	BRHIP2010487//	91.660	//	0	//	0.000
	BRHIP2010571//	0	//	0.000	//	18.366
35	BRHIP2011491//	0	//	0.000	//	0.986
	BRHIP2011616//	0	//	0.000	//	53.896

	BRHIP2015245//	0	//	0.000	//	5.663
	BRHIP2018712//	0	//	0.000	//	9.661
	BRHIP2019149//	0	//	0.000	//	13.172
	BRHIP2020799//	0	//	0.000	//	12.072
5	BRHIP2021762//	0	//	0.000	//	6.646
	BRHIP2022228//	0	//	0.000	//	10.898
	BRHIP2022326//	0	//	0.000	//	1.015
	BRHIP2023888//	0	//	0.000	//	0.439
	BRHIP2024742//	0	//	0.000	//	1.487
10	BRHIP2024911//	0	//	0.000	//	11.054
	BRHIP2027017//	0	//	0.000	//	13.730
	BRHIP3000017//	0	//	0.000	//	15.777
	BRHIP3000377//	0	//	0.000	//	6.870
	BRHIP3001076//	0	//	0.000	//	53.896
15	BRHIP3002141//	0	//	0.000	//	18.713
	BRHIP3005307//	0	//	0.000	//	53.896
	BRHIP3007223//	0	//	0.000	//	2.405
	BRHIP3007586//	0	//	0.000	//	4.116
	BRHIP3008344//	0	//	0.000	//	53.896
20	BRHIP3008565//	0	//	0.000	//	53.896
	BRHIP3012997//	0	//	87.379	//	0.000
	BRHIP3017855//	0	//	0.000	//	27.401
	BRHIP3020046//	0	//	0.000	//	1.208
	BRSSN2000295//	0	//	0.000	//	8.260
25	BRSSN2000498//	0	//	0.000	//	2.610
	BRSSN2001213//	0	//	0.000	//	24.268
	BRSSN2001869//	0	//	0.000	//	3.600
	BRSSN2006892//	0	//	0.000	//	18.468
	BRSSN2009518//	0	//	0.000	//	2.054
30	BRSSN2010019//	0	//	0.000	//	13.842
	BRSSN2014685//	0	//	0.000	//	16.936
	BRSSN2017422//	0	//	0.000	//	17.148
	BRSTN2001067//	0	//	0.000	//	7.384
	BRSTN2010089//	0	//	0.000	//	7.869
35	BRSTN2011961//	0	//	0.000	//	0.345
	BRSTN2012069//	3.583	//	1.784	//	0.271

	BRSTN2012174//	0	//	0.000	//	0.482
	BRSTN2013502//	0	//	0.000	//	5.797
	BRSTN2013931//	0	//	0.000	//	3.457
	BRSTN2016470//	0	//	0.000	//	0.522
5	BRSTN2016892//	0	//	0.000	//	3.559
	BRTHA2000057//	0	//	0.000	//	51.819
	BRTHA2004361//	0	//	0.000	//	51.819
	BRTHA2005831//	0	//	0.000	//	51.819
	BRTHA2005864//	0	//	0.000	//	1.935
10	BRTHA2010608//	0	//	0.000	//	51.819
	BRTHA2012183//	0	//	0.000	//	51.819
	BRTHA2012714//	0	//	0.000	//	5.980
	BRTHA2017178//	0	//	0.000	//	51.819
	BRTHA3003023//	0	//	0.000	//	2.410
15	BRTHA3003074//	0	//	0.000	//	13.429
	BRTHA3003736//	0	//	0.000	//	5.131
	BRTHA3004307//	0	//	0.000	//	17.964
	BRTHA3011265//	0	//	0.000	//	10.176
	BRTHA3020314//	0	//	0.000	//	12.144
20	BRTHA3023403//	0	//	0.000	//	26.579
	BRTHA3026507//	0	//	0.000	//	4.167
	BRTHA3027879//	0	//	0.000	//	51.819
	CHONS2002829//	0	//	0.000	//	11.691
	CTONG1000052//	0	//	0.000	//	2.162
25	CTONG1000087//	0	//	0.000	//	2.494
	CTONG1000094//	0	//	0.000	//	0.464
	CTONG1000137//	0	//	0.000	//	39.037
	CTONG1000180//	0	//	0.000	//	28.641
	CTONG1000241//	0	//	0.000	//	7.590
30	CTONG1000277//	0	//	0.000	//	24.668
	CTONG1000467//	0	//	0.000	//	10.248
	CTONG2000411//	0	//	0.000	//	6.864
	CTONG2000508//	0	//	0.000	//	4.709
	CTONG2001748//	0	//	0.000	//	2.493
35	CTONG2001932//	0	//	0.000	//	12.322
	CTONG2002073//	32.643	//	0	//	1.747

	CTONG2002270// 0 // 0.000 // 0.633
	CTONG2002744// 0 // 0.000 // 0.702
	CTONG2002766// 0 // 0.000 // 14.092
	CTONG2002803// 32.814 // 0 // 0.000
5	CTONG2003298// 0 // 0.000 // 1.731
	CTONG2003348// 0 // 0.000 // 39.037
	CTONG2003517// 0 // 0.000 // 13.371
	CTONG2003524// 0 // 0.000 // 1.922
	CTONG2004423// 0 // 0.000 // 13.705
10	CTONG2005145// 0 // 0.000 // 29.265
	CTONG2005615// 0 // 0.000 // 5.671
	CTONG2006235// 0 // 0.000 // 1.954
	CTONG2006377// 0 // 0.000 // 14.002
	CTONG2006562// 0 // 0.000 // 5.010
15	CTONG2006932// 0 // 0.000 // 2.625
	CTONG2007078// 0 // 0.000 // 3.048
	CTONG2007500// 0 // 0.000 // 8.072
	CTONG2008343// 0 // 0.000 // 39.037
	CTONG2008398// 0 // 0.000 // 0.912
20	CTONG2008518// 0 // 0.000 // 4.593
	CTONG2008689// 0 // 0.000 // 24.924
	CTONG2009529// 0 // 0.000 // 7.541
	CTONG2009923// 0 // 0.000 // 39.037
	CTONG2009938// 0 // 0.000 // 23.863
25	CTONG2010348// 0 // 0.000 // 6.336
	CTONG2010408// 0 // 0.000 // 10.219
	CTONG2010649// 0 // 0.000 // 5.595
	CTONG2010821// 0 // 0.000 // 2.557
	CTONG2011801// 0 // 0.000 // 3.532
30	CTONG2011825// 0 // 0.000 // 10.239
	CTONG2012452// 7.936 // 0 // 0.000
	CTONG2012847// 38.378 // 0 // 2.054
	CTONG2012879// 0 // 0.000 // 4.056
	CTONG2012996// 0 // 0.000 // 3.482
35	CTONG2013128// 0 // 0.000 // 39.037
	CTONG2013156// 0 // 0.000 // 24.668

	CTONG2013907//	0	//	0.000	//	2.571
	CTONG2013934//	0	//	0.000	//	8.273
	CTONG2014369//	0	//	0.000	//	4.963
	CTONG2014898//	0	//	0.000	//	13.759
5	CTONG2015345//	0	//	0.000	//	10.182
	CTONG2016056//	0	//	0.000	//	2.372
	CTONG2016408//	0	//	0.000	//	4.416
	CTONG2016575//	0	//	0.000	//	1.779
	CTONG2016869//	0	//	0.000	//	3.150
10	CTONG2017094//	0	//	0.000	//	2.666
	CTONG2017429//	0	//	0.000	//	8.607
	CTONG2017998//	0	//	0.000	//	5.976
	CTONG2018211//	0	//	0.000	//	4.068
	CTONG2018637//	0	//	0.000	//	15.649
15	CTONG2018898//	0	//	0.000	//	2.298
	CTONG2019822//	0	//	0.000	//	7.755
	CTONG2020378//	0	//	0.000	//	19.250
	CTONG2020411//	0	//	0.000	//	32.844
	CTONG2020484//	0	//	55.423	//	0.000
20	CTONG2020560//	0	//	0.000	//	5.368
	CTONG2024031//	0	//	0.000	//	6.165
	CTONG2027263//	0	//	0.000	//	19.641
	CTONG2028124//	0	//	0.000	//	2.997
	CTONG3001123//	0	//	0.000	//	9.359
25	CTONG3002518//	0	//	0.000	//	10.064
	CTONG3004317//	0	//	0.000	//	39.037
	CTONG3008894//	0	//	0.000	//	0.867
	CTONG3009028//	0	//	0.000	//	3.839
	CTONG3009239//	0	//	0.000	//	1.722
30	D30ST3000258//	0	//	0.000	//	22.242
	D60ST2000464//	0	//	0.000	//	1.307
	D90ST2002608//	0	//	0.000	//	2.657
	D90ST2003791//	0	//	0.000	//	7.297
	DFNES1000185//	29.393	//	0	//	0.000
35	DFNES2000011//	0	//	0.000	//	4.565
	DFNES2000426//	0	//	0.000	//	15.059

	DFNES2000443//	0	//	0.000	//	0.810
	DFNES2001829//	0	//	0.000	//	11.006
	DFNES2006346//	0	//	0.000	//	8.425
	DFNES2007634//	0	//	0.000	//	7.421
5	FCBBF1000024//	0	//	0.000	//	5.237
	FCBBF1000027//	0	//	0.000	//	2.621
	FCBBF1000061//	0	//	0.000	//	2.805
	FCBBF1000182//	0	//	0.000	//	10.114
	FCBBF1000197//	0	//	0.000	//	2.548
10	FCBBF1000294//	0	//	0.000	//	1.284
	FCBBF1000367//	0	//	0.000	//	1.812
	FCBBF1000412//	0	//	0.000	//	2.308
	FCBBF1000425//	0	//	0.000	//	6.226
	FCBBF1000466//	14.193	//	0	//	0.760
15	FCBBF1000574//	0	//	0.000	//	4.952
	FCBBF1000760//	0	//	0.000	//	0.781
	FCBBF2000087//	0	//	0.000	//	3.441
	FCBBF2000591//	0	//	0.000	//	0.342
	FCBBF2000685//	0	//	0.000	//	8.114
20	FCBBF2000885//	0	//	0.000	//	3.661
	FCBBF2001001//	0	//	0.000	//	11.399
	FCBBF2001291//	0	//	0.000	//	2.269
	FCBBF2006380//	0	//	0.000	//	39.231
	FCBBF3000115//	0	//	0.000	//	9.520
25	FCBBF3000536//	0	//	0.000	//	3.179
	FCBBF3001470//	0	//	0.000	//	1.619
	FCBBF3003800//	0	//	0.000	//	1.409
	FCBBF3004473//	25.604	//	0	//	1.370
	FCBBF3004847//	0	//	0.000	//	39.231
30	FCBBF3006821//	0	//	0.000	//	13.636
	FCBBF3007244//	0	//	0.000	//	9.258
	FCBBF3007859//	0	//	0.000	//	7.748
	FCBBF3008153//	0	//	0.000	//	6.525
	FCBBF3010695//	0	//	0.000	//	2.958
35	FCBBF3016928//	0	//	0.000	//	1.045
	FCBBF3017396//	0	//	0.000	//	7.305

	FCBBF3017531//	0	//	0.000	//	1.912
	FCBBF3018796//	0	//	0.000	//	7.405
	FCBBF3019714//	0	//	0.000	//	2.443
	FCBBF3019839//	0	//	0.000	//	17.866
5	FCBBF3021807//	0	//	0.000	//	5.171
	FCBBF3023667//	0	//	0.000	//	0.317
	FCBBF3024002//	0	//	0.000	//	6.769
	FCBBF3024623//	0	//	0.000	//	6.682
	FCBBF3025528//	0	//	0.000	//	5.758
10	FCBBF3025568//	0	//	0.000	//	19.615
	FCBBF3025737//	0	//	0.000	//	7.752
	FCBBF3025905//	0	//	0.000	//	19.079
	FCBBF4000142//	0	//	0.000	//	4.360
	FCBBF4000446//	0	//	0.000	//	0.896
15	FCBBF5000261//	0	//	0.000	//	6.193
	FEBRA1000022//	0	//	0.000	//	12.554
	FEBRA1000088//	0	//	0.000	//	5.090
	FEBRA2000105//	0	//	0.000	//	1.711
	FEBRA2000129//	0	//	0.000	//	3.100
20	FEBRA2000210//	0	//	0.000	//	0.843
	FEBRA2000462//	0	//	0.000	//	6.733
	FEBRA2000510//	0	//	0.000	//	4.401
	FEBRA2000536//	0	//	0.000	//	3.757
	FEBRA2000581//	0	//	0.000	//	0.949
25	FEBRA2000680//	0	//	0.000	//	33.628
	FEBRA2000733//	3.756	//	0	//	1.206
	FEBRA2000740//	0	//	0.000	//	9.442
	FEBRA2000757//	0	//	0.000	//	3.652
	FEBRA2000856//	0	//	0.000	//	18.931
30	FEBRA2000880//	0	//	0.000	//	12.639
	FEBRA2001745//	0	//	0.000	//	1.495
	FEBRA2001828//	0	//	0.000	//	6.489
	FEBRA2002527//	0	//	0.000	//	3.416
	FEBRA2003436//	0	//	0.000	//	6.630
35	FEBRA2003750//	0	//	0.000	//	19.596
	FEBRA2003833//	0	//	0.000	//	14.436

	FEBRA2003926//	0	//	0.000	//	4.163
	FEBRA2004042//	47.274	//	0	//	0.000
	FEBRA2004412//	0	//	0.000	//	3.502
	FEBRA2004852//	0	//	0.000	//	32.361
5	FEBRA2005752//	0	//	0.000	//	4.964
	FEBRA2006092//	0	//	0.000	//	2.225
	FEBRA2007714//	0	//	0.000	//	9.952
	FEBRA2007818//	0	//	0.000	//	6.669
	FEBRA2007901//	0	//	0.000	//	4.420
10	FEBRA2008081//	0	//	0.000	//	0.845
	FEBRA2008087//	3.995	//	0	//	0.214
	FEBRA2008210//	0	//	0.000	//	15.999
	FEBRA2008255//	0	//	0.000	//	6.035
	FEBRA2008302//	0	//	0.000	//	1.269
15	FEBRA2008583//	0	//	0.000	//	0.315
	FEBRA2009419//	0	//	0.000	//	1.576
	FEBRA2011090//	0	//	0.000	//	20.700
	FEBRA2011392//	0	//	0.000	//	32.361
	FEBRA2014417//	0	//	0.000	//	1.288
20	FEBRA2022055//	0	//	0.000	//	5.712
	FEBRA2022504//	0	//	0.000	//	1.959
	FEBRA2023927//	0	//	0.000	//	4.858
	FEBRA2025838//	0	//	0.000	//	0.980
	FEBRA2026984//	0	//	0.000	//	20.914
25	FEBRA2028516//	0	//	0.000	//	1.364
	FELIV1000153//	0	//	0.000	//	0.197
	HCASM2000016//	0	//	0.000	//	1.780
	HCASM2000138//	0	//	0.000	//	10.075
	HCASM2000363//	0	//	0.000	//	0.811
30	HCASM2001890//	0	//	0.000	//	15.228
	HCASM2008536//	0	//	0.000	//	15.228
	HCHON1000030//	0	//	0.000	//	0.216
	HCHON1000131//	0	//	0.000	//	9.787
	HCHON1000142//	0	//	0.000	//	15.860
35	HCHON2000056//	0	//	0.000	//	1.353
	HCHON2000087//	0	//	58.329	//	0.738

	HCHON2000160//	0	//	0.000	//	1.201
	HCHON2000226//	0	//	0.000	//	0.962
	HCHON2000244//	0	//	0.000	//	1.569
	HCHON2000265//	0	//	0.000	//	2.413
5	HCHON2000295//	0	//	0.000	//	1.045
	HCHON2000323//	0	//	0.000	//	2.209
	HCHON2000418//	0	//	0.000	//	15.860
	HCHON2000475//	0	//	0.000	//	3.175
	HCHON2000626//	0	//	0.000	//	5.608
10	HCHON2000698//	0	//	0.000	//	10.256
	HCHON2000738//	0	//	0.000	//	3.551
	HCHON2000743//	0	//	0.000	//	7.282
	HCHON2000826//	0	//	0.000	//	0.854
	HCHON2001039//	0	//	0.000	//	2.662
15	HCHON2001084//	0	//	0.000	//	2.739
	HCHON2001200//	0	//	40.779	//	1.032
	HCHON2001217//	0	//	0.000	//	4.966
	HCHON2001434//	0	//	0.000	//	3.644
	HCHON2001505//	0	//	0.000	//	16.079
20	HCHON2001598//	0	//	0.000	//	5.796
	HCHON2001665//	0	//	0.000	//	1.840
	HCHON2001853//	0	//	0.000	//	6.680
	HCHON2002247//	0	//	0.000	//	3.348
	HCHON2004002//	0	//	0.000	//	0.936
25	HCHON2005921//	0	//	0.000	//	24.732
	HCHON2006250//	34.872	//	0	//	0.000
	HCHON2007650//	0	//	0.000	//	7.263
	HCHON2008444//	0	//	0.000	//	15.860
	HEART1000149//	0	//	0.000	//	4.480
30	HEART1000185//	0	//	0.000	//	5.657
	HEART2000506//	0	//	0.000	//	4.183
	HEART2004931//	0	//	0.000	//	8.110
	HEART2007231//	0	//	0.000	//	11.555
	HHDP1000114//	0	//	0.000	//	0.867
35	HHDP1000163//	0	//	0.000	//	1.500
	HHDP2000455//	0	//	0.000	//	3.932

	HHDPC2000572//	0	//	0.000	//	7.809
	HHDPC2000656//	0	//	0.000	//	10.195
	HHDPC2003439//	0	//	0.000	//	1.517
	HHDPC2003983//	0	//	0.000	//	2.657
5	HHDPC2007267//	0	//	0.000	//	0.582
	HHDPC2007775//	0	//	0.000	//	12.888
	HLUNG1000055//	0	//	0.000	//	1.937
	HLUNG1000064//	0	//	0.000	//	8.121
	HLUNG1000076//	0	//	0.000	//	1.003
10	HLUNG2000004//	0	//	0.000	//	3.017
	HLUNG2000063//	0	//	0.000	//	5.883
	HLUNG2000314//	0	//	0.000	//	5.852
	HLUNG2000412//	0	//	0.000	//	3.194
	HLUNG2000501//	0	//	0.000	//	1.023
15	HLUNG2000846//	0	//	0.000	//	5.388
	HLUNG2000884//	0	//	0.000	//	2.553
	HLUNG2001146//	0	//	0.000	//	6.252
	HLUNG2001507//	0	//	0.000	//	5.972
	HLUNG2001518//	0	//	0.000	//	5.217
20	HLUNG2001677//	0	//	0.000	//	4.191
	HLUNG2002648//	0	//	0.000	//	4.311
	HLUNG2002811//	0	//	0.000	//	2.906
	HLUNG2003003//	0	//	0.000	//	28.594
	HLUNG2004159//	0	//	0.000	//	2.162
25	HLUNG2004170//	0	//	0.000	//	7.349
	HLUNG2004684//	75.236	//	0	//	0.000
	HLUNG2006812//	0	//	0.000	//	7.053
	HLUNG2008333//	0	//	0.000	//	24.539
	HLUNG2008637//	0	//	0.000	//	2.015
30	HLUNG2009225//	0	//	0.000	//	5.396
	HLUNG2015184//	0	//	0.000	//	15.617
	HLUNG2017262//	0	//	0.000	//	3.783
	HSYRA1000062//	0	//	0.000	//	0.511
	HSYRA1000152//	0	//	0.000	//	1.423
35	HSYRA1000178//	0	//	0.000	//	2.991
	HSYRA2000159//	0	//	0.000	//	0.719

	HSYRA2000224//	0	//	0.000	//	2.145
	HSYRA2000232//	0	//	0.000	//	0.882
	HSYRA2000248//	0	//	0.000	//	4.053
	HSYRA2000255//	0	//	0.000	//	2.141
5	HSYRA2000640//	0	//	0.000	//	4.064
	HSYRA2000743//	0	//	0.000	//	10.153
	HSYRA2001105//	0	//	0.000	//	3.286
	HSYRA2001138//	0	//	0.000	//	0.304
	HSYRA2001396//	0	//	0.000	//	5.436
10	HSYRA2001476//	0	//	0.000	//	5.182
	HSYRA2001567//	0	//	0.000	//	2.673
	HSYRA2001574//	0	//	0.000	//	0.897
	HSYRA2001580//	0	//	0.000	//	13.073
	HSYRA2001615//	0	//	0.000	//	2.473
15	HSYRA2001621//	0	//	17.301	//	0.000
	HSYRA2007650//	0	//	0.000	//	5.673
	IMR321000158//	0	//	0.000	//	1.816
	IMR321000210//	0	//	0.000	//	1.209
	IMR321000219//	0	//	0.000	//	3.013
20	IMR321000242//	0	//	0.000	//	6.707
	IMR321000266//	0	//	0.000	//	3.375
	IMR322000121//	0	//	0.000	//	1.330
	IMR322000730//	3.055	//	0	//	0.327
	IMR322000935//	0	//	0.000	//	1.786
25	IMR322001049//	0	//	0.000	//	6.909
	IMR322001435//	0	//	0.000	//	3.361
	IMR322001534//	0	//	0.000	//	9.855
	IMR322001600//	0	//	15.181	//	0.960
	IMR322001710//	0	//	0.000	//	2.313
30	IMR322001879//	0	//	0.000	//	11.495
	IMR322019070//	0	//	0.000	//	3.191
	KIDNE1000036//	0	//	0.000	//	25.490
	KIDNE1000145//	0	//	0.000	//	16.491
	KIDNE2000085//	0	//	0.000	//	3.679
35	KIDNE2000330//	76.084	//	0	//	0.000
	KIDNE2000403//	0	//	0.000	//	1.971

	KIDNE2001162//	0	//	0.000	//	1.670
	KIDNE2001467//	0	//	0.000	//	0.933
	KIDNE2001979//	0	//	0.000	//	7.027
	KIDNE2002252//	0	//	0.000	//	2.600
5	KIDNE2003305//	0	//	0.000	//	1.004
	KIDNE2003941//	0	//	0.000	//	0.602
	KIDNE2005321//	0	//	0.000	//	11.785
	KIDNE2005676//	0	//	0.000	//	5.034
	KIDNE2006014//	0	//	0.000	//	3.541
10	KIDNE2006030//	0	//	0.000	//	7.636
	KIDNE2006248//	0	//	0.000	//	1.112
	KIDNE2006465//	0	//	0.000	//	3.690
	KIDNE2007040//	0	//	0.000	//	25.490
	KIDNE2007328//	0	//	0.000	//	2.110
15	KIDNE2007352//	0	//	0.000	//	0.992
	KIDNE2007811//	0	//	0.000	//	10.218
	KIDNE2007954//	0	//	0.000	//	2.514
	KIDNE2008048//	0	//	0.000	//	3.839
	KIDNE2009367//	0	//	0.000	//	9.888
20	KIDNE2009605//	0	//	0.000	//	18.012
	KIDNE2010049//	76.623	//	0	//	4.101
	KIDNE2012784//	0	//	0.000	//	40.625
	KIDNE2013158//	0	//	0.000	//	21.635
	KIDNE2013845//	0	//	0.000	//	2.666
25	KIDNE2014290//	0	//	0.000	//	3.345
	KIDNE2014325//	0	//	0.000	//	4.512
	KIDNE2017040//	0	//	0.000	//	4.011
	LIVER1000079//	0	//	0.000	//	2.090
	LIVER1000132//	0	//	0.000	//	0.597
30	LIVER2000033//	0	//	0.000	//	1.650
	LIVER2001539//	0	//	0.000	//	5.939
	LIVER2001608//	29.267	//	0	//	1.566
	LIVER2002842//	0	//	0.000	//	9.107
	LIVER2003234//	0	//	0.000	//	12.095
35	LIVER2005218//	0	//	0.000	//	5.883
	LIVER2007783//	0	//	0.000	//	4.894

	LIVER2008465//	0	//	0.000	//	7.893
	MAMGL1000083//	0	//	0.000	//	0.346
	MESAN2000264//	0	//	0.000	//	2.350
	MESAN2000267//	0	//	0.000	//	2.930
5	MESAN2000894//	0	//	0.000	//	24.337
	MESAN2001154//	0	//	0.000	//	1.589
	MESAN2002086//	0	//	0.000	//	2.482
	MESAN2002424//	0	//	0.000	//	24.337
	MESAN2002724//	0	//	0.000	//	5.499
10	MESAN2002844//	0	//	0.000	//	8.642
	MESAN2003039//	0	//	0.000	//	19.415
	MESAN2003058//	0	//	0.000	//	7.143
	MESAN2003444//	0	//	0.000	//	8.886
	MESAN2003709//	0	//	0.000	//	9.892
15	MESAN2005303//	0	//	0.000	//	9.449
	MESAN2005957//	0	//	0.000	//	17.666
	MESAN2006043//	0	//	0.000	//	9.499
	MESAN2006580//	0	//	0.000	//	24.337
	MESAN2006743//	0	//	0.000	//	13.792
20	MESAN2009580//	0	//	0.000	//	1.325
	MESAN2013284//	0	//	0.000	//	2.930
	MESAN2014295//	0	//	0.000	//	24.337
	MESAN2016552//	0	//	0.000	//	14.511
	MESAN2017152//	0	//	0.000	//	24.337
25	NB9N41000121//	16.735	//	0	//	0.000
	NB9N42000281//	0	//	0.000	//	2.280
	NOVAR1000015//	0	//	0.000	//	3.622
	NOVAR1000091//	0	//	0.000	//	2.310
	NOVAR2000710//	0	//	0.000	//	4.201
30	NT2NE1000163//	0	//	0.000	//	2.899
	NT2NE2000056//	8.755	//	0	//	3.280
	NT2NE2000327//	0	//	0.000	//	3.000
	NT2NE2000383//	0	//	0.000	//	5.437
	NT2NE2000384//	0	//	0.000	//	2.745
35	NT2NE2000455//	0	//	0.000	//	24.761
	NT2NE2000575//	0	//	0.000	//	1.720

	NT2NE2000707//	0	//	0.000	//	1.596
	NT2NE2000963//	5.112	//	0	//	0.547
	NT2NE2001000//	0	//	0.000	//	2.053
	NT2NE2001176//	0	//	0.000	//	1.362
5	NT2NE2001337//	0	//	0.000	//	5.420
	NT2NE2001435//	0	//	0.000	//	5.072
	NT2NE2001545//	0	//	0.000	//	2.137
	NT2NE2001617//	0	//	0.000	//	5.411
	NT2NE2001660//	0	//	0.000	//	9.341
10	NT2NE2001793//	0	//	0.000	//	7.422
	NT2NE2002620//	0	//	90.183	//	0.000
	NT2NE2003185//	0	//	0.000	//	4.521
	NT2NE2003485//	0	//	0.000	//	5.552
	NT2NE2003569//	0	//	0.000	//	2.070
15	NT2NE2004519//	0	//	0.000	//	2.137
	NT2NE2004716//	0	//	0.000	//	4.578
	NT2NE2005358//	0	//	0.000	//	24.761
	NT2NE2006458//	0	//	0.000	//	3.372
	NT2NE2006659//	0	//	0.000	//	21.581
20	NT2NE2009295//	0	//	0.000	//	2.379
	NT2NE2015974//	0	//	0.000	//	9.111
	NT2NE2017492//	0	//	0.000	//	20.127
	NT2RI1000127//	0	//	0.000	//	2.165
	NT2RI2000007//	0	//	0.000	//	39.625
25	NT2RI2000064//	0	//	0.000	//	3.210
	NT2RI2000282//	0	//	0.000	//	0.378
	NT2RI2000294//	0	//	0.000	//	2.257
	NT2RI2000344//	0	//	76.334	//	0.000
	NT2RI2000578//	7.452	//	31.528	//	0.399
30	NT2RI2000671//	0	//	0.000	//	1.255
	NT2RI2000685//	0	//	0.000	//	3.545
	NT2RI2000689//	34.460	//	0	//	1.844
	NT2RI2000727//	0	//	0.000	//	0.617
	NT2RI2001091//	0	//	0.000	//	4.193
35	NT2RI2001230//	0	//	0.000	//	0.920
	NT2RI2001540//	1.269	//	0	//	1.494

	NT2RI2001657//	0	//	0.000	//	1.914
	NT2RI2001859//	0	//	0.000	//	1.157
	NT2RI2002091//	0.897	//	2.529	//	0.976
	NT2RI2002152//	0	//	0.000	//	3.000
5	NT2RI2002316//	0	//	0.000	//	0.956
	NT2RI2002391//	18.073	//	0	//	0.000
	NT2RI2002654//	13.092	//	0	//	0.000
	NT2RI2002865//	0	//	0.000	//	8.087
	NT2RI2003304//	5.848	//	0	//	0.000
10	NT2RI2003317//	0	//	0.000	//	3.760
	NT2RI2003338//	0	//	0.000	//	4.831
	NT2RI2003344//	0	//	0.000	//	6.968
	NT2RI2003407//	0	//	0.000	//	1.444
	NT2RI2003420//	0	//	0.000	//	1.837
15	NT2RI2003556//	0	//	0.000	//	0.908
	NT2RI2003695//	0	//	0.000	//	0.939
	NT2RI2003738//	0	//	0.000	//	1.252
	NT2RI2003751//	0	//	0.000	//	1.652
	NT2RI2004157//	0	//	0.000	//	39.625
20	NT2RI2004188//	0	//	0.000	//	3.425
	NT2RI2004230//	0	//	0.000	//	6.843
	NT2RI2004535//	0	//	0.000	//	2.283
	NT2RI2005116//	0	//	0.000	//	1.525
	NT2RI2005335//	0	//	0.000	//	3.232
25	NT2RI2005358//	0	//	0.000	//	24.478
	NT2RI2005405//	0	//	0.000	//	1.004
	NT2RI2005713//	0	//	0.000	//	1.764
	NT2RI2005723//	11.184	//	0	//	1.197
	NT2RI2005811//	0	//	0.000	//	1.827
30	NT2RI2005814//	0	//	0.000	//	1.553
	NT2RI2005818//	0	//	0.000	//	3.038
	NT2RI2006412//	0	//	0.000	//	0.978
	NT2RI2006825//	0	//	0.000	//	3.270
	NT2RI2007054//	0	//	0.000	//	3.097
35	NT2RI2007148//	0	//	0.000	//	2.253
	NT2RI2007277//	0	//	0.000	//	1.169

	NT2R12007384//	9.651	//	0	//	1.033
	NT2R12007445//	0	//	0.000	//	2.139
	NT2R12007498//	0	//	0.000	//	0.486
	NT2R12007589//	23.800	//	0	//	0.000
5	NT2R12007629//	0	//	0.000	//	2.404
	NT2R12007987//	0	//	0.000	//	2.147
	NT2R12008007//	0	//	0.000	//	23.084
	NT2R12008045//	0	//	0.000	//	0.926
	NT2R12008336//	0	//	0.000	//	0.956
10	NT2R12008481//	0	//	0.000	//	2.646
	NT2R12008526//	17.086	//	0	//	0.000
	NT2R12008724//	0	//	0.000	//	2.190
	NT2R12008749//	0	//	0.000	//	2.023
	NT2R12008791//	0	//	0.000	//	1.392
15	NT2R12008942//	0	//	0.000	//	16.259
	NT2R12009037//	0	//	0.000	//	1.005
	NT2R12009065//	10.408	//	0	//	0.000
	NT2R12009269//	0	//	0.000	//	1.179
	NT2R12009402//	0	//	0.000	//	7.482
20	NT2R12009406//	0	//	0.000	//	3.356
	NT2R12009583//	0	//	0.000	//	0.267
	NT2R12014247//	0	//	0.000	//	18.191
	NT2R12014733//	0	//	0.000	//	29.743
	NT2R12017529//	0	//	0.000	//	1.157
25	NT2R12022468//	0	//	0.000	//	7.995
	NT2R12024313//	0	//	0.000	//	17.475
	NT2R12027323//	0	//	0.000	//	39.625
	NT2R13001445//	0	//	0.000	//	7.554
	NT2R13005724//	0	//	0.000	//	7.069
30	NT2R13005923//	0	//	0.000	//	23.249
	NT2R13006284//	46.111	//	0	//	0.000
	NT2R13006340//	0	//	0.000	//	19.479
	NT2R13006666//	0	//	0.000	//	24.901
	NT2R13006673//	0	//	0.000	//	11.902
35	NT2R13007291//	0	//	0.000	//	14.928
	NT2R13007543//	0	//	0.000	//	1.012

	NT2RP6000017//	0	//	0.000	//	3.569
	NT2RP6000039//	0	//	0.000	//	4.277
	NT2RP6000059//	0	//	0.000	//	25.869
	NT2RP6000077//	0	//	0.000	//	30.666
5	NT2RP6000078//	0	//	0.000	//	0.429
	NT2RP6000085//	0	//	0.000	//	11.032
	NT2RP6000123//	0	//	0.000	//	0.467
	NT2RP7000069//	0	//	0.000	//	8.035
	NT2RP7000076//	0	//	0.000	//	0.727
10	NT2RP7000173//	0	//	0.000	//	0.663
	NT2RP7000477//	0	//	0.000	//	2.360
	NT2RP7000586//	0	//	0.000	//	13.104
	NT2RP7000600//	0	//	0.000	//	7.929
	NT2RP7000906//	0	//	0.000	//	3.112
15	NT2RP7001166//	0	//	0.000	//	2.676
	NT2RP7001962//	0	//	0.000	//	3.168
	NT2RP7002028//	0	//	0.000	//	7.190
	NT2RP7002376//	0	//	0.000	//	14.471
	NT2RP7002379//	0	//	0.000	//	2.402
20	NT2RP7002449//	0	//	0.000	//	2.409
	NT2RP7002802//	0	//	0.000	//	8.717
	NT2RP7002875//	0	//	0.000	//	1.101
	NT2RP7002982//	0	//	0.000	//	9.273
	NT2RP7003055//	0	//	0.000	//	12.585
25	NT2RP7003203//	0	//	0.000	//	4.406
	NT2RP7003319//	0	//	0.000	//	31.557
	NT2RP7003632//	0	//	0.000	//	1.942
	NT2RP7003647//	0	//	0.000	//	5.615
	NT2RP7003688//	0	//	0.000	//	0.881
30	NT2RP7004114//	0	//	0.000	//	6.650
	NT2RP7004123//	0	//	0.000	//	2.289
	NT2RP7004196//	0	//	0.000	//	1.563
	NT2RP7004348//	0	//	0.000	//	2.695
	NT2RP7004352//	0	//	0.000	//	6.077
35	NT2RP7004373//	0	//	0.000	//	2.807
	NT2RP7004559//	0	//	0.000	//	10.166

	NT2RP7004728//	0	//	0.000	//	1.875
	NT2RP7004751//	0	//	44.129	//	1.116
	NT2RP7004915//	0	//	0.000	//	17.708
	NT2RP7004925//	0	//	0.000	//	1.506
5	NT2RP7004946//	0	//	0.000	//	2.053
	NT2RP7005513//	0	//	0.000	//	2.016
	NT2RP7005529//	0	//	0.000	//	8.806
	NT2RP7005675//	0	//	0.000	//	10.406
	NT2RP7005750//	0	//	0.000	//	4.268
10	NT2RP7006223//	0	//	0.000	//	5.039
	NT2RP7006490//	0	//	0.000	//	2.560
	NT2RP7006539//	0	//	0.000	//	10.410
	NT2RP7006619//	0	//	0.000	//	2.633
	NT2RP7006717//	0	//	0.000	//	5.493
15	NT2RP7006886//	0	//	0.000	//	11.344
	NT2RP7007114//	0	//	0.000	//	19.540
	NT2RP7007154//	0	//	0.000	//	1.360
	NT2RP7007252//	0	//	0.000	//	8.190
	NT2RP7007310//	82.993	//	0	//	0.000
20	NT2RP7007381//	0	//	0.000	//	18.704
	NT2RP7007537//	27.403	//	0	//	0.000
	NT2RP7007610//	0	//	0.000	//	3.452
	NT2RP7008161//	0	//	0.000	//	7.488
	NT2RP7008167//	0	//	0.000	//	2.165
25	NT2RP7008190//	0	//	0.000	//	1.582
	NT2RP7008315//	0	//	0.000	//	8.950
	NT2RP7008543//	0	//	0.000	//	3.281
	NT2RP7009087//	0	//	0.000	//	2.897
	NT2RP7009097//	40.067	//	0	//	0.000
30	NT2RP7009147//	0	//	0.000	//	1.900
	NT2RP7009259//	0	//	0.000	//	2.010
	NT2RP7009482//	0	//	0.000	//	5.527
	NT2RP7010612//	0	//	0.000	//	25.799
	NT2RP7013573//	0	//	0.000	//	8.594
35	NT2RP7017474//	0	//	0.000	//	22.450
	NTONG1000033//	0	//	0.000	//	1.461

	NTONG1000098//	0	//	0.000	//	0.760
	NTONG1000182//	0	//	0.000	//	1.477
	NTONG1000246//	0	//	0.000	//	1.865
	NTONG2000265//	0	//	0.000	//	1.017
5	NTONG2000876//	0	//	0.000	//	1.661
	NTONG2001550//	0	//	0.000	//	4.151
	NTONG2001567//	0	//	0.000	//	1.097
	NTONG2002582//	0	//	0.000	//	13.457
	NTONG2003454//	0	//	0.000	//	24.889
10	NTONG2003839//	0	//	0.000	//	6.254
	NTONG2004844//	0	//	0.000	//	1.933
	NTONG2005363//	0	//	0.000	//	13.929
	NTONG2005391//	0	//	0.000	//	13.902
	NTONG2005520//	0	//	0.000	//	0.794
15	NTONG2005801//	0	//	0.000	//	4.250
	NTONG2005897//	0	//	0.000	//	8.187
	NTONG2008944//	0	//	0.000	//	6.965
	OCBBF1000086//	0	//	0.000	//	1.826
	OCBBF1000175//	0	//	0.000	//	8.591
20	OCBBF2000015//	17.632	//	0	//	3.774
	OCBBF2000467//	0	//	0.000	//	2.406
	OCBBF2000677//	0	//	0.000	//	19.428
	OCBBF2000986//	0	//	0.000	//	1.149
	OCBBF2001166//	0	//	0.000	//	6.537
25	OCBBF2001210//	0	//	0.000	//	4.324
	OCBBF2001323//	0	//	0.000	//	10.255
	OCBBF2001586//	0	//	0.000	//	8.553
	OCBBF2001961//	0	//	0.000	//	48.981
	OCBBF2002086//	0	//	0.000	//	15.370
30	OCBBF2002656//	0	//	0.000	//	1.973
	OCBBF2003246//	0	//	0.000	//	11.672
	OCBBF2003925//	0	//	0.000	//	0.994
	OCBBF2004273//	19.976	//	0	//	0.000
	OCBBF2004757//	0	//	0.000	//	2.956
35	OCBBF2005476//	0	//	0.000	//	16.727
	OCBBF2005956//	0	//	0.000	//	3.386

	OCBBF2006313//	0	//	0.000	//	6.810
	OCBBF2006849//	0	//	0.000	//	2.410
	OCBBF2007028//	0	//	0.000	//	8.234
	OCBBF2007415//	0	//	0.000	//	0.955
5	OCBBF2007829//	0	//	0.000	//	7.203
	OCBBF2008005//	0	//	0.000	//	3.787
	OCBBF2008144//	0	//	0.000	//	3.440
	OCBBF2009242//	0	//	0.000	//	3.377
	OCBBF2009301//	46.196	//	0	//	0.000
10	OCBBF2009424//	0	//	0.000	//	8.655
	OCBBF2009772//	0	//	0.000	//	1.404
	OCBBF2010313//	0	//	0.000	//	16.359
	OCBBF2010557//	0	//	0.000	//	43.708
	OCBBF2010830//	0	//	0.000	//	2.099
15	OCBBF2010945//	0	//	0.000	//	48.981
	OCBBF2011021//	0	//	0.000	//	1.724
	OCBBF2011228//	0	//	0.000	//	25.500
	OCBBF2011232//	0	//	0.000	//	9.556
	OCBBF2011536//	0	//	0.000	//	2.379
20	OCBBF2011759//	0	//	0.000	//	3.344
	OCBBF2013149//	0	//	0.000	//	1.850
	OCBBF2013843//	0	//	50.379	//	0.637
	OCBBF2014064//	0	//	0.000	//	3.258
	OCBBF2014292//	0	//	0.000	//	3.706
25	OCBBF2017398//	0	//	0.000	//	3.068
	OCBBF2017754//	0	//	0.000	//	8.956
	OCBBF2017791//	0	//	0.000	//	9.166
	OCBBF2017882//	0	//	0.000	//	8.510
	OCBBF2018012//	0	//	0.000	//	10.043
30	OCBBF2018563//	0	//	0.000	//	24.528
	OCBBF2018873//	0	//	0.000	//	6.611
	OCBBF2018956//	0	//	0.000	//	2.019
	OCBBF2020741//	0	//	0.000	//	33.655
	OCBBF2021833//	0	//	0.000	//	17.297
35	OCBBF2024850//	0	//	0.000	//	26.505
	OCBBF2026368//	0	//	0.000	//	19.710

	OCBBF2027148//	0	//	0.000	//	27.753
	OCBBF2036743//	0	//	0.000	//	13.183
	OCBBF3001333//	0	//	0.000	//	3.832
	OCBBF3004487//	0	//	0.000	//	5.404
5	PEBLM1000144//	0	//	0.000	//	7.153
	PEBLM2000030//	0	//	0.000	//	4.390
	PEBLM2000147//	0	//	0.000	//	1.522
	PEBLM2000326//	0	//	0.000	//	6.474
	PEBLM2004452//	0	//	0.000	//	6.439
10	PEBLM2006366//	0	//	0.000	//	3.301
	PEBLM2006709//	0	//	0.000	//	6.636
	PERIC2006443//	0	//	0.000	//	5.792
	PERIC2007068//	0	//	0.000	//	5.521
	PLACE5000013//	0	//	0.000	//	9.466
15	PLACE5000113//	0	//	0.000	//	10.260
	PLACE5000159//	0	//	0.000	//	8.132
	PLACE5000170//	0	//	0.000	//	4.147
	PLACE5000372//	0	//	0.000	//	40.126
	PLACE6000145//	23.096	//	0	//	0.000
20	PLACE6000263//	0	//	0.000	//	1.813
	PLACE6000379//	0	//	0.000	//	1.264
	PLACE6000414//	0	//	0.000	//	6.113
	PLACE6001064//	0	//	0.000	//	3.421
	PLACE6001185//	0	//	0.000	//	25.473
25	PLACE6001281//	0	//	0.000	//	4.106
	PLACE6001443//	0	//	0.000	//	11.713
	PLACE6001886//	0	//	0.000	//	40.398
	PLACE6002084//	0	//	0.000	//	0.881
	PLACE6002102//	0	//	0.000	//	6.738
30	PLACE6002668//	0	//	0.000	//	6.437
	PLACE6002960//	0	//	0.000	//	2.647
	PLACE6003218//	0	//	0.000	//	17.355
	PLACE6003383//	0	//	0.000	//	1.424
	PLACE6004005//	0	//	0.000	//	1.178
35	PLACE6004312//	0	//	0.000	//	0.719
	PLACE6004397//	0	//	0.000	//	2.192

	PLACE6004491// 0 // 0.000 // 40.126
	PLACE6004738// 0 // 0.000 // 25.098
	PLACE6005482// 0 // 0.000 // 22.076
	PLACE6006042// 0 // 0.000 // 6.493
5	PLACE6006137// 0 // 0.000 // 4.074
	PLACE6006186// 0 // 0.000 // 25.880
	PLACE6006549// 0 // 0.000 // 1.905
	PLACE6008775// 0 // 0.000 // 6.595
	PLACE6008824// 0 // 0.000 // 40.126
10	PLACE6009338// 0 // 0.000 // 29.967
	PLACE6010077// 0 // 0.000 // 2.077
	PLACE6011057// 0 // 0.000 // 2.688
	PLACE6012942// 0 // 0.000 // 40.126
	PLACE6015731// 0 // 0.000 // 18.307
15	PLACE6016383// 0 // 0.000 // 7.710
	PLACE6017431// 0 // 0.000 // 40.126
	PLACE6018938// 0 // 0.000 // 18.301
	PLACE7006240// 0 // 0.000 // 30.024
	PROST1000097// 0 // 0.000 // 7.013
20	PROST1000199// 16.283 // 0 // 4.357
	PROST1000220// 0 // 0.000 // 0.810
	PROST1000226// 0 // 0.000 // 2.134
	PROST1000246// 0 // 0.000 // 13.104
	PROST1000526// 0 // 0.000 // 3.013
25	PROST1000564// 0 // 0.000 // 1.603
	PROST2000138// 5.795 // 0 // 5.479
	PROST2000273// 0 // 0.000 // 25.167
	PROST2002651// 0 // 0.000 // 7.133
	PROST2003232// 0 // 0.000 // 0.814
30	PROST2003338// 0 // 0.000 // 4.005
	PROST2003396// 0 // 0.000 // 7.125
	PROST2004095// 0 // 0.000 // 1.116
	PROST2004258// 0 // 0.000 // 9.101
	PROST2004270// 0 // 0.000 // 2.104
35	PROST2004416// 0 // 0.000 // 0.811
	PROST2005285// 0 // 0.000 // 8.902

	PROST2005604//	0	//	0.000	//	7.420
	PROST2006030//	0	//	0.000	//	4.513
	PROST2006536//	0	//	0.000	//	2.647
	PROST2006737//	0	//	0.000	//	8.672
5	PROST2007200//	0	//	0.000	//	14.088
	PROST2008271//	0	//	0.000	//	4.674
	PROST2008489//	14.433	//	0	//	0.772
	PROST2008770//	0	//	0.000	//	0.930
	PROST2010318//	0	//	0.000	//	14.395
10	PROST2010545//	0	//	0.000	//	15.696
	PROST2010782//	0	//	0.000	//	0.290
	PROST2012007//	0	//	0.000	//	1.354
	PROST2012448//	0	//	0.000	//	9.731
	PROST2012890//	0	//	0.000	//	18.191
15	PROST2014916//	0	//	0.000	//	4.345
	PROST2015924//	0	//	0.000	//	8.082
	PROST2016918//	0	//	0.000	//	15.159
	PROST2017203//	0	//	0.000	//	1.549
	PROST2017617//	0	//	0.000	//	25.167
20	PROST2017692//	0	//	0.000	//	0.879
	PROST2018977//	0	//	0.000	//	15.499
	PUAEN1000057//	0	//	0.000	//	7.346
	PUAEN1000065//	0	//	0.000	//	1.598
	PUAEN1000164//	0	//	0.000	//	0.475
25	PUAEN1000239//	0	//	0.000	//	3.697
	PUAEN2000374//	0	//	0.000	//	1.145
	PUAEN2001586//	0	//	0.000	//	3.406
	PUAEN2007044//	0	//	0.000	//	1.710
	PUAEN2008228//	0	//	0.000	//	17.449
30	PUAEN2009655//	0	//	0.000	//	4.359
	SALGL1000157//	0	//	0.000	//	0.465
	SKMUS1000014//	0	//	0.000	//	8.773
	SKMUS1000022//	0	//	0.000	//	0.496
	SKMUS1000084//	0	//	0.000	//	3.674
35	SKMUS1000138//	0	//	0.000	//	0.344
	SKMUS1000177//	0	//	0.000	//	14.082

	SKMUS1000186//	0	//	0.000	//	0.479
	SKMUS2000020//	0	//	0.000	//	4.393
	SKMUS2000343//	0	//	0.000	//	18.379
	SKMUS2000361//	0	//	0.000	//	1.275
5	SKMUS2000380//	0	//	0.000	//	2.586
	SKMUS2000873//	0	//	0.000	//	1.312
	SKMUS2000902//	0	//	0.000	//	12.901
	SKMUS2000931//	0	//	0.000	//	0.649
	SKMUS2000954//	0	//	0.000	//	2.027
10	SKMUS2001129//	0	//	0.000	//	12.130
	SKMUS2001454//	7.522	//	0	//	0.403
	SKMUS2001501//	0	//	0.000	//	2.600
	SKNMC1000110//	0	//	0.000	//	4.318
	SKNMC1000137//	0	//	0.000	//	1.264
15	SKNMC1000168//	0	//	0.000	//	1.997
	SKNMC1000251//	0	//	0.000	//	8.366
	SKNMC2000065//	0	//	0.000	//	2.575
	SKNMC2000097//	0	//	0.000	//	1.063
	SKNMC2000305//	0	//	0.000	//	4.201
20	SKNMC2000635//	0	//	0.000	//	0.856
	SKNMC2000649//	0	//	0.000	//	2.176
	SKNMC2000877//	0	//	0.000	//	2.827
	SKNSH1000086//	0	//	0.000	//	10.184
	SKNSH2000347//	0	//	0.000	//	8.028
25	SKNSH2000482//	0	//	0.000	//	23.251
	SKNSH2000819//	0	//	0.000	//	5.937
	SKNSH2002325//	0	//	0.000	//	4.553
	SKNSH2003528//	0	//	0.000	//	3.621
	SKNSH2008043//	0	//	0.000	//	12.076
30	SMINT1000042//	59.707	//	0	//	6.391
	SMINT1000100//	0	//	0.000	//	6.640
	SMINT1000117//	0	//	0.000	//	1.569
	SMINT1000131//	0	//	0.000	//	3.277
	SMINT2000159//	0	//	0.000	//	6.518
35	SMINT2000277//	0	//	0.000	//	2.162
	SMINT2000396//	0	//	0.000	//	5.840

	SMINT2000441// 0 // 0.000 // 1.615
	SMINT2000468// 0 // 0.000 // 5.458
	SMINT2000545// 0 // 0.000 // 2.827
	SMINT2000629// 0 // 0.000 // 3.203
5	SMINT2001950// 0 // 0.000 // 12.743
	SMINT2002159// 0 // 0.000 // 8.177
	SMINT2002314// 53.944 // 0 // 0.000
	SMINT2002689// 0 // 0.000 // 51.875
	SMINT2002778// 0 // 0.000 // 25.261
10	SMINT2002976// 0 // 0.000 // 6.221
	SMINT2003169// 0 // 0.000 // 0.561
	SMINT2004589// 0 // 0.000 // 4.780
	SMINT2005368// 0 // 0.000 // 1.401
	SMINT2005956// 0 // 0.000 // 6.278
15	SMINT2006801// 0 // 0.000 // 19.209
	SMINT2007187// 0 // 0.000 // 8.007
	SMINT2008960// 0 // 0.000 // 0.816
	SMINT2010959// 0 // 0.000 // 18.459
	SMINT2011033// 0 // 0.000 // 25.261
20	SMINT2012122// 0 // 0.000 // 4.169
	SMINT2013031// 0 // 0.000 // 7.403
	SMINT2013695// 0 // 0.000 // 25.261
	SMINT2014480// 35.406 // 0 // 0.000
	SMINT2018681// 0 // 0.000 // 4.988
25	SPLN1000106// 0 // 0.000 // 13.880
	SPLN1000116// 0 // 0.000 // 0.590
	SPLN1000166// 0 // 0.000 // 2.696
	SPLN2000243// 0 // 0.000 // 25.928
	SPLN2000255// 0 // 0.000 // 5.495
30	SPLN2000505// 0 // 0.000 // 0.503
	SPLN2000839// 0 // 0.000 // 10.886
	SPLN2001141// 0 // 0.000 // 2.253
	SPLN2001157// 0 // 0.000 // 3.280
	SPLN2001689// 0 // 0.000 // 16.646
35	SPLN2002335// 0 // 0.000 // 6.038
	SPLN2002463// 0 // 0.000 // 9.032

	SPLEN2003297//	0	//	0.000	//	31.668
	SPLEN2004220//	0	//	0.000	//	3.430
	SPLEN2005009//	0	//	0.000	//	10.253
	SPLEN2005429//	0	//	0.000	//	17.478
5	SPLEN2005927//	0	//	0.000	//	5.136
	SPLEN2006122//	18.769	//	0	//	0.000
	SPLEN2006133//	21.141	//	0	//	2.263
	SPLEN2006143//	0	//	0.000	//	2.668
	SPLEN2006232//	0	//	0.000	//	3.421
10	SPLEN2006305//	0	//	0.000	//	1.507
	SPLEN2006374//	0	//	0.000	//	5.438
	SPLEN2007388//	0	//	0.000	//	31.668
	SPLEN2007498//	0	//	0.000	//	3.121
	SPLEN2009315//	0	//	0.000	//	40.674
15	SPLEN2010195//	0	//	0.000	//	4.164
	SPLEN2011419//	0	//	0.000	//	2.850
	SPLEN2011737//	0	//	0.000	//	3.107
	SPLEN2012571//	0	//	0.000	//	3.792
	SPLEN2012800//	0	//	0.000	//	0.407
20	SPLEN2013690//	0	//	0.000	//	12.880
	SPLEN2014080//	0	//	0.000	//	5.651
	SPLEN2014572//	0	//	0.000	//	7.423
	SPLEN2016268//	9.628	//	0	//	0.000
	SPLEN2016421//	0	//	0.000	//	2.471
25	SPLEN2016554//	0	//	0.000	//	22.228
	SPLEN2016972//	0	//	0.000	//	4.837
	SPLEN2017318//	0	//	0.000	//	6.052
	SPLEN2017918//	0	//	0.000	//	3.262
	SPLEN2018098//	0	//	0.000	//	40.674
30	SPLEN2018157//	0	//	0.000	//	5.754
	SPLEN2019169//	0	//	0.000	//	6.752
	SPLEN2019311//	0	//	0.000	//	57.827
	SPLEN2019405//	0	//	0.000	//	3.416
	SPLEN2021194//	0	//	0.000	//	8.047
35	SPLEN2021273//	0	//	0.000	//	17.589
	SPLEN2022522//	0	//	0.000	//	1.691

	SPLEN2027113//	0	//	0.000	//	1.952
	SPLEN2028466//	0	//	0.000	//	0.987
	SPLEN2031547//	0	//	0.000	//	5.633
	SPLEN2036932//	0	//	0.000	//	3.497
5	SPLEN2039379//	0	//	0.000	//	10.362
	SPLEN2041585//	0	//	0.000	//	40.674
	SPLEN2042714//	0	//	0.000	//	40.674
	STOMA1000186//	0	//	0.000	//	14.912
	STOMA1000189//	0	//	0.000	//	1.865
10	STOMA2000289//	0	//	0.000	//	6.498
	STOMA2000395//	0	//	0.000	//	5.092
	STOMA2000396//	0	//	0.000	//	6.147
	STOMA2002052//	0	//	0.000	//	6.634
	STOMA2004925//	0	//	0.000	//	14.912
15	SYNOV1000124//	0	//	0.000	//	1.327
	SYNOV2001033//	0	//	0.000	//	0.715
	SYNOV2001239//	6.992	//	0	//	0.374
	SYNOV2001262//	0	//	0.000	//	4.977
	SYNOV2017055//	0	//	0.000	//	20.136
20	SYNOV4000598//	0	//	0.000	//	35.608
	SYNOV4001224//	0	//	0.000	//	35.608
	SYNOV4001395//	0	//	0.000	//	21.660
	SYNOV4009575//	0	//	0.000	//	5.715
	T1ESE2000904//	0	//	0.000	//	2.754
25	TBAES2000059//	0	//	0.000	//	1.797
	TBAES2003702//	0	//	0.000	//	14.497
	TBAES2009387//	0	//	0.000	//	0.638
	TCERX2000613//	0	//	0.000	//	14.497
	TESOP2002273//	0	//	0.000	//	4.841
30	TESOP2006893//	0	//	0.000	//	10.246
	TESTI1000023//	0	//	0.000	//	2.000
	TESTI2000184//	0	//	0.000	//	4.045
	TESTI2000356//	0	//	0.000	//	20.914
	TESTI2000784//	0	//	0.000	//	5.421
35	TESTI2000970//	0	//	0.000	//	5.798
	TESTI2001099//	0	//	0.000	//	4.091

	TESTI2001153//	0	//	0.000	//	5.699
	TESTI2001420//	0	//	0.000	//	64.596
	TESTI2001829//	0	//	0.000	//	1.013
	TESTI2001862//	0	//	0.000	//	3.154
5	TESTI2002149//	0	//	0.000	//	3.990
	TESTI2002365//	0	//	0.000	//	3.907
	TESTI2002632//	0	//	0.000	//	12.913
	TESTI2002877//	0	//	0.000	//	44.500
	TESTI2003005//	0	//	0.000	//	3.623
10	TESTI2003533//	0	//	0.000	//	1.034
	TESTI2004031//	8.934	//	0	//	0.478
	TESTI2004295//	0	//	0.000	//	9.766
	TESTI2004737//	0	//	0.000	//	2.113
	TESTI2004929//	0	//	0.000	//	3.386
15	TESTI2005731//	0	//	0.000	//	3.941
	TESTI2005759//	0	//	0.000	//	2.231
	TESTI2005908//	0	//	0.000	//	1.878
	TESTI2006051//	0	//	0.000	//	0.505
	TESTI2006111//	0	//	0.000	//	24.590
20	TESTI2006588//	0	//	0.000	//	4.520
	TESTI2007211//	0	//	0.000	//	3.939
	TESTI2007407//	0	//	0.000	//	7.322
	TESTI2008240//	0	//	0.000	//	2.982
	TESTI2008835//	0	//	0.000	//	12.941
25	TESTI2009520//	0	//	0.000	//	0.894
	TESTI2009577//	0	//	0.000	//	2.108
	TESTI2009785//	0	//	0.000	//	6.845
	TESTI2010513//	8.756	//	0	//	1.874
	TESTI2011683//	0	//	0.000	//	38.615
30	TESTI2014838//	0	//	0.000	//	3.160
	TESTI2015213//	0	//	0.000	//	0.612
	TESTI2015626//	7.329	//	0	//	0.784
	TESTI2017954//	0	//	0.000	//	0.790
	TESTI2018462//	0	//	0.000	//	3.370
35	TESTI2020871//	0	//	0.000	//	64.596
	TESTI2021124//	0	//	0.000	//	6.816

	TESTI2021358// 0 // 0.000 // 40.357
	TESTI2021425// 0 // 0.000 // 4.107
	TESTI2027165// 0 // 0.000 // 64.596
	TESTI2029259// 73.757 // 0 // 3.947
5	TESTI2033441// 0 // 0.000 // 2.618
	TESTI2034940// 0 // 0.000 // 1.864
	TESTI2036913// 0 // 0.000 // 24.204
	TESTI2036969// 0 // 0.000 // 4.285
	TESTI2039177// 0 // 0.000 // 4.943
10	TESTI2044788// 0 // 0.000 // 64.596
	TESTI2046456// 0 // 0.000 // 1.104
	TESTI2047605// 0 // 0.000 // 17.379
	TESTI2053723// 0 // 0.000 // 5.399
	TESTI4000014// 0 // 0.000 // 0.639
15	TESTI4001467// 0 // 0.000 // 6.603
	TESTI4002072// 0 // 0.000 // 3.983
	TESTI4002195// 0 // 0.000 // 15.959
	TESTI4002799// 9.842 // 0 // 1.053
	TESTI4003703// 0 // 0.000 // 5.277
20	TESTI4003944// 0 // 0.000 // 41.606
	TESTI4005399// 0 // 0.000 // 9.300
	TESTI4005534// 0 // 0.000 // 33.259
	TESTI4008797// 0 // 0.000 // 14.824
	TESTI4009286// 0 // 0.000 // 2.594
25	TESTI4013441// 0 // 14.788 // 0.374
	TESTI4013675// 0 // 0.000 // 35.326
	TESTI4013894// 0 // 0.000 // 33.408
	TESTI4014159// 0 // 0.000 // 13.979
	TESTI4018886// 0 // 0.000 // 64.596
30	TESTI4024245// 0 // 0.000 // 40.205
	TESTI4029671// 0 // 0.000 // 22.183
	TESTI4037156// 0 // 0.000 // 1.320
	TESTI4038284// 41.043 // 0 // 0.000
	THYMU1000002// 13.191 // 0 // 0.000
35	THYMU1000016// 0 // 0.000 // 2.304
	THYMU1000041// 0 // 0.000 // 5.672

	THYMU1000083// 0 // 0.000 // 10.729
	THYMU1000103// 0 // 0.000 // 2.103
	THYMU1000109// 0 // 0.000 // 0.939
	THYMU1000142// 0 // 0.000 // 58.853
5	THYMU1000316// 0 // 0.000 // 58.853
	THYMU1000359// 0 // 0.000 // 1.918
	THYMU1000374// 0 // 0.000 // 3.573
	THYMU1000394// 0 // 0.000 // 11.726
	THYMU1000428// 0 // 0.000 // 0.678
10	THYMU2000382// 0 // 0.000 // 2.892
	THYMU2000436// 20.534 // 0 // 1.099
	THYMU2000684// 0 // 0.000 // 4.966
	THYMU2001007// 0 // 0.000 // -6.471
	THYMU2001422// 0 // 0.000 // 14.855
15	THYMU2002583// 0 // 0.000 // 0.618
	THYMU2002815// 0 // 0.000 // 39.408
	THYMU2003012// 0 // 0.000 // 2.090
	THYMU2003046// 0 // 0.000 // 4.585
	THYMU2003419// 0 // 0.000 // 3.594
20	THYMU2003446// 0 // 0.000 // 2.845
	THYMU2003891// 0 // 0.000 // 0.174
	THYMU2003981// 0 // 0.000 // 2.491
	THYMU2004152// 0 // 0.000 // 1.184
	THYMU2004410// 0 // 0.000 // 2.285
25	THYMU2005546// 12.190 // 0 // 0.000
	THYMU2006505// 0 // 0.000 // 6.513
	THYMU2006813// 0 // 0.000 // 1.887
	THYMU2007415// 0 // 0.000 // 8.658
	THYMU2007467// 0 // 0.000 // 4.818
30	THYMU2007886// 30.859 // 0 // 0.000
	THYMU2008686// 0 // 0.000 // 14.535
	THYMU2008725// 0 // 0.000 // 15.552
	THYMU2009658// 0 // 0.000 // 0.418
	THYMU2010094// 0 // 0.000 // 6.947
35	THYMU2010448// 0 // 0.000 // 6.315
	THYMU2012024// 0 // 0.000 // 3.554

	THYMU2013916//	0	//	0.000	//	2.646
	THYMU2015321//	0	//	0.000	//	58.853
	THYMU2019021//	0	//	0.000	//	5.796
	THYMU2020667//	0	//	0.000	//	41.697
5	THYMU2021684//	0	//	0.000	//	58.853
	THYMU2024071//	0	//	0.000	//	39.309
	THYMU2025319//	0	//	0.000	//	39.408
	THYMU2031890//	0	//	0.000	//	21.176
	THYMU2033070//	0	//	0.000	//	58.853
10	THYMU2034917//	0	//	0.000	//	23.175
	THYMU2035735//	0	//	0.000	//	11.014
	THYMU2036461//	0	//	0.000	//	18.090
	THYMU3001472//	0	//	0.000	//	20.097
	THYMU3002578//	0	//	0.000	//	36.487
15	THYMU3013386//	0	//	0.000	//	1.786
	THYMU3021586//	0	//	0.000	//	4.926
	THYMU3026350//	0	//	0.000	//	17.045
	THYMU3028410//	0	//	0.000	//	58.853
	THYMU3032798//	0	//	0.000	//	2.306
20	THYMU3034616//	0	//	0.000	//	58.853
	THYMU3034671//	0	//	0.000	//	19.911
	TOVAR2000476//	50.572	//	0	//	0.000
	TRACH1000030//	0	//	0.000	//	5.760
	TRACH1000038//	0	//	0.000	//	8.984
25	TRACH1000063//	0	//	0.000	//	2.565
	TRACH1000181//	0	//	0.000	//	5.650
	TRACH1000205//	0	//	0.000	//	4.694
	TRACH2000079//	0	//	0.000	//	0.646
	TRACH2000237//	0	//	0.000	//	6.412
30	TRACH2000248//	0	//	0.000	//	2.496
	TRACH2000321//	0	//	0.000	//	2.344
	TRACH2000359//	0	//	0.000	//	3.557
	TRACH2000461//	0	//	0.000	//	2.045
	TRACH2000472//	0	//	0.000	//	9.166
35	TRACH2000780//	0	//	0.000	//	5.212
	TRACH2000959//	0	//	0.000	//	0.582

	TRACH2001021// 9.332 // 0 // 1.498
	TRACH2001192// 0 // 0.000 // 40.205
	TRACH2001289// 0 // 0.000 // 1.622
	TRACH2001432// 0 // 0.000 // 1.327
5	TRACH2001443// 0 // 0.000 // 11.083
	TRACH2001463// 0 // 0.000 // 3.652
	TRACH2001549// 0 // 0.000 // 5.043
	TRACH2001596// 0 // 0.000 // 24.409
	TRACH2001612// 0 // 0.000 // 4.764
10	TRACH2001810// 0 // 0.000 // 0.926
	TRACH2002054// 0 // 0.000 // 51.568
	TRACH2002537// 0 // 0.000 // 2.212
	TRACH2003272// 0 // 0.000 // 4.419
	TRACH2003323// 0 // 0.000 // 2.123
15	TRACH2005811// 0 // 0.000 // 1.258
	TRACH2007399// 0 // 0.000 // 1.685
	TRACH2008300// 0 // 0.000 // 2.025
	TRACH2014124// 0 // 0.000 // 3.693
	TRACH2014442// 50.173 // 0 // 0.000
20	TRACH2014997// 0 // 0.000 // 25.316
	TRACH2015823// 0 // 0.000 // 5.218
	TRACH2016481// 0 // 0.000 // 51.568
	TRACH2017609// 0 // 0.000 // 37.903
	TRACH2018950// 0 // 0.000 // 17.915
25	TRACH3000692// 0 // 0.000 // 5.590
	TRACH3002192// 0 // 0.000 // 4.463
	TRACH3003379// 0 // 0.000 // 29.185
	TRACH3003547// 0 // 0.000 // 5.044
	TRACH3003872// 0 // 0.000 // 9.820
30	TRACH3004068// 0 // 0.000 // 1.700
	TRACH3004721// 0 // 0.000 // 3.467
	TRACH3005699// 0 // 0.000 // 22.893
	TRACH3006800// 0 // 0.000 // 34.742
	TRACH3007479// 0 // 0.000 // 3.848
35	TRACH3008632// 0 // 0.000 // 20.157
	TRACH3009008// 0 // 0.000 // 5.843

	TRACH3009148//	0	//	0.000	//	10.698
	TUTER1000014//	100.000	//	0	//	0.000
	TUTER1000122//	72.738	//	0	//	0.000
	TUTER1000137//	95.706	//	0	//	0.000
5	TUTER2000057//	92.461	//	0	//	0.000
	TUTER2000283//	100.000	//	0	//	0.000
	TUTER2000425//	100.000	//	0	//	0.000
	TUTER2000904//	62.217	//	0	//	3.330
	TUTER2000916//	100.000	//	0	//	0.000
10	TUTER2001286//	100.000	//	0	//	0.000
	TUTER2001341//	100.000	//	0	//	0.000
	TUTER2001387//	100.000	//	0	//	0.000
	TUTER2001433//	100.000	//	0	//	0.000
	TUTER2001461//	100.000	//	0	//	0.000
15	TUTER2002028//	100.000	//	0	//	0.000
	TUTER2002074//	100.000	//	0	//	0.000
	TUTER2002158//	100.000	//	0	//	0.000
	TUTER2002228//	100.000	//	0	//	0.000
	TUTER2002323//	72.582	//	0	//	0.000
20	TUTER2002356//	100.000	//	0	//	0.000
	TUTER2002729//	100.000	//	0	//	0.000
	UMVEN1000122//	0	//	92.143	//	0.000
	UMVEN1000143//	0	//	77.431	//	0.000
	UMVEN1000156//	0	//	97.424	//	0.000
25	UMVEN1000186//	0	//	74.732	//	0.630
	UMVEN2000046//	0	//	100.000	//	0.000
	UMVEN2000069//	0	//	100.000	//	0.000
	UMVEN2000121//	0	//	97.690	//	0.000
	UMVEN2000133//	0	//	55.263	//	2.097
30	UMVEN2000152//	0	//	74.264	//	0.000
	UMVEN2000354//	0	//	77.661	//	0.000
	UMVEN2000453//	0	//	49.229	//	1.245
	UTERU1000000//	0	//	0.000	//	58.°53
	UTERU1000015//	0	//	0.000	//	100.000
35	UTERU1000024//	0	//	0.000	//	100.000
	UTERU1000031//	0	//	0.000	//	100.000

	UTERU1000032//	0	//	0.000	//	100.000
	UTERU1000057//	0	//	0.000	//	100.000
	UTERU1000065//	0	//	0.000	//	100.000
	UTERU1000077//	0	//	0.000	//	100.000
5	UTERU1000093//	0	//	0.000	//	100.000
	UTERU1000096//	0	//	0.000	//	24.268
	UTERU1000106//	0	//	0.000	//	6.873
	UTERU1000109//	0	//	0.000	//	100.000
	UTERU1000131//	0	//	0.000	//	100.000
10	UTERU1000138//	0	//	0.000	//	100.000
	UTERU1000148//	0	//	0.000	//	100.000
	UTERU1000160//	0	//	0.000	//	100.000
	UTERU1000182//	0	//	0.000	//	1.935
	UTERU1000183//	0	//	0.000	//	100.000
15	UTERU1000187//	0	//	0.000	//	100.000
	UTERU1000192//	0	//	0.000	//	100.000
	UTERU1000249//	0	//	0.000	//	100.000
	UTERU1000337//	0	//	0.000	//	100.000
	UTERU1000339//	0	//	0.000	//	100.000
20	UTERU1000384//	0	//	0.000	//	8.500
	UTERU2000023//	0	//	0.000	//	24.419
	UTERU2000047//	0	//	0.000	//	100.000
	UTERU2000074//	0	//	0.000	//	62.692
	UTERU2000095//	0	//	0.000	//	0.987
25	UTERU2000099//	0	//	0.000	//	100.000
	UTERU2000154//	0	//	0.000	//	100.000
	UTERU2000197//	0	//	0.000	//	39.231
	UTERU2000218//	0	//	0.000	//	100.000
	UTERU2000238//	0	//	0.000	//	100.000
30	UTERU2000243//	0	//	0.000	//	100.000
	UTERU2000260//	0	//	0.000	//	24.831
	UTERU2000263//	0	//	0.000	//	2.444
	UTERU2000300//	0	//	0.000	//	11.765
	UTERU2000329//	0	//	0.000	//	68.264
35	UTERU2000332//	0	//	0.000	//	5.640
	UTERU2000338//	0	//	0.000	//	3.979

	UTERU2000349//	0	//	0.000	//	100.000
	UTERU2000377//	0	//	0.000	//	100.000
	UTERU2000393//	0	//	0.000	//	100.000
	UTERU2000418//	0	//	0.000	//	34.205
5	UTERU2000424//	0	//	0.000	//	1.013
	UTERU2000465//	0	//	0.000	//	100.000
	UTERU2000485//	0	//	0.000	//	15.228
	UTERU2000517//	0	//	0.000	//	100.000
	UTERU2000524//	0	//	0.000	//	100.000
10	UTERU2000537//	0	//	0.000	//	12.239
	UTERU2000539//	0	//	0.000	//	100.000
	UTERU2000541//	0	//	0.000	//	7.522
	UTERU2000542//	0	//	0.000	//	10.769
	UTERU2000546//	0	//	0.000	//	100.000
15	UTERU2000550//	0	//	0.000	//	100.000
	UTERU2000569//	0	//	0.000	//	100.000
	UTERU2000607//	0	//	0.000	//	100.000
	UTERU2000629//	0	//	0.000	//	100.000
	UTERU2000649//	0	//	0.000	//	100.000
20	UTERU2000663//	0	//	0.000	//	100.000
	UTERU2000696//	63.416	//	0	//	3.394
	UTERU2000794//	0	//	0.000	//	100.000
	UTERU2000830//	0	//	0.000	//	100.000
	UTERU2000844//	0	//	0.000	//	100.000
25	UTERU2000922//	0	//	0.000	//	100.000
	UTERU2000925//	0	//	0.000	//	12.420
	UTERU2001024//	0	//	0.000	//	100.000
	UTERU2001110//	0	//	0.000	//	24.268
	UTERU2001176//	0	//	0.000	//	100.000
30	UTERU2001281//	0	//	0.000	//	100.000
	UTERU2001389//	0	//	0.000	//	100.000
	UTERU2001409//	0	//	0.000	//	100.000
	UTERU2001412//	0	//	0.000	//	100.000
	UTERU2001504//	0	//	0.000	//	100.000
35	UTERU2001607//	0	//	0.000	//	1.759
	UTERU2001658//	0	//	0.000	//	10.564

	UTERU2001747//	0	//	0.000	//	100.000
	UTERU2001876//	0	//	0.000	//	100.000
	UTERU2002001//	0	//	0.000	//	40.126
	UTERU2002011//	0	//	0.000	//	100.000
5	UTERU2002176//	0	//	0.000	//	100.000
	UTERU2002198//	0	//	0.000	//	64.596
	UTERU2002294//	0	//	0.000	//	2.165
	UTERU2002332//	0	//	0.000	//	100.000
	UTERU2002410//	13.085	//	0	//	0.700
10	UTERU2002473//	0	//	0.000	//	100.000
	UTERU2002547//	0	//	0.000	//	100.000
	UTERU2002662//	0	//	0.000	//	4.244
	UTERU2002693//	0	//	0.000	//	100.000
	UTERU2002733//	0	//	0.000	//	100.000
15	UTERU2002736//	0	//	0.000	//	100.000
	UTERU2002737//	0	//	0.000	//	100.000
	UTERU2002826//	82.260	//	0	//	4.402
	UTERU2002841//	0	//	0.000	//	64.596
	UTERU2002964//	0	//	0.000	//	25.187
20	UTERU2002993//	0	//	0.000	//	64.596
	UTERU2003035//	0	//	0.000	//	100.000
	UTERU2003057//	0	//	0.000	//	3.085
	UTERU2003126//	0	//	0.000	//	100.000
	UTERU2003135//	0	//	0.000	//	100.000
25	UTERU2003321//	0	//	0.000	//	47.706
	UTERU2003399//	0	//	0.000	//	100.000
	UTERU2003411//	0	//	0.000	//	0.360
	UTERU2003456//	0	//	0.000	//	12.899
	UTERU2003577//	0	//	0.000	//	100.000
30	UTERU2003704//	0	//	0.000	//	20.529
	UTERU2003926//	0	//	0.000	//	40.126
	UTERU2003973//	0	//	0.000	//	100.000
	UTERU2004015//	0	//	0.000	//	100.000
	UTERU2004037//	0	//	0.000	//	5.230
35	UTERU2004039//	0	//	0.000	//	100.000
	UTERU2004061//	0	//	0.000	//	100.000

	UTERU2004073// 0 // 0.000 // 23.318
	UTERU2004163// 0 // 0.000 // 100.000
	UTERU2004197// 0 // 0.000 // 4.796
	UTERU2004299// 0 // 0.000 // 100.000
5	UTERU2004461// 0 // 0.000 // 32.361
	UTERU2004520// 0 // 0.000 // 39.037
	UTERU2004564// 0 // 0.000 // 100.000
	UTERU2004664// 0 // 0.000 // 4.048
	UTERU2004688// 0 // 0.000 // 6.630
10	UTERU2004698// 0 // 0.000 // 100.000
	UTERU2004807// 0 // 0.000 // 17.972
	UTERU2004861// 0 // 0.000 // 56.434
	UTERU2004929// 0 // 0.000 // 13.845
	UTERU2005004// 0 // 0.000 // 41.697
15	UTERU2005050// 0 // 0.000 // 100.000
	UTERU2005069// 0 // 0.000 // 64.596
	UTERU2005074// 0 // 0.000 // 27.087
	UTERU2005179// 0 // 0.000 // 100.000
	UTERU2005292// 0 // 0.000 // 3.714
20	UTERU2005346// 0 // 0.000 // 100.000
	UTERU2005354// 0 // 0.000 // 2.609
	UTERU2005446// 0 // 0.000 // 24.816
	UTERU2005449// 0 // 0.000 // 19.526
	UTERU2005450// 0 // 0.000 // 100.000
25	UTERU2005533// 0 // 0.000 // 100.000
	UTERU2005593// 0 // 0.000 // 4.016
	UTERU2005601// 0 // 0.000 // 3.040
	UTERU2005621// 0 // 0.000 // 5.377
	UTERU2005664// 0 // 0.000 // 13.328
30	UTERU2005822// 0 // 0.000 // 100.000
	UTERU2005903// 0 // 0.000 // 100.000
	UTERU2005905// 0 // 0.000 // 100.000
	UTERU2006103// 0 // 0.000 // 100.000
	UTERU2006115// 0 // 0.000 // 9.347
35	UTERU2006137// 0 // 0.000 // 9.269
	UTERU2006182// 0 // 0.000 // 100.000

	UTERU2006400//	0	//	0.000	//	15.228
	UTERU2006412//	0	//	0.000	//	100.000
	UTERU2006429//	0	//	0.000	//	100.000
	UTERU2006486//	0	//	0.000	//	51.819
5	UTERU2006524//	0	//	0.000	//	53.896
	UTERU2006547//	0	//	0.000	//	24.268
	UTERU2006568//	0	//	0.000	//	100.000
	UTERU2006593//	0	//	0.000	//	3.522
	UTERU2006643//	0	//	0.000	//	10.128
10	UTERU2006651//	0	//	0.000	//	100.000
	UTERU2006705//	0	//	0.000	//	100.000
	UTERU2006899//	0	//	0.000	//	100.000
	UTERU2007004//	0	//	0.000	//	24.856
	UTERU2007075//	0	//	0.000	//	100.000
15	UTERU2007081//	0	//	0.000	//	17.449
	UTERU2007128//	0	//	0.000	//	100.000
	UTERU2007253//	0	//	0.000	//	12.290
	UTERU2007267//	0	//	0.000	//	100.000
	UTERU2007444//	0	//	0.000	//	64.596
20	UTERU2007499//	0	//	0.000	//	100.000
	UTERU2007639//	0	//	0.000	//	100.000
	UTERU2007724//	0	//	0.000	//	15.672
	UTERU2007924//	0	//	0.000	//	3.190
	UTERU2007942//	0	//	0.000	//	100.000
25	UTERU2008018//	0	//	0.000	//	24.856
	UTERU2008019//	0	//	0.000	//	100.000
	UTERU2008027//	0	//	0.000	//	4.562
	UTERU2008040//	0	//	0.000	//	14.037
	UTERU2008077//	0	//	0.000	//	100.000
30	UTERU2008085//	0	//	0.000	//	0.323
	UTERU2008130//	0	//	0.000	//	53.896
	UTERU2008302//	0	//	0.000	//	3.187
	UTERU2008347//	0	//	0.000	//	100.000
	UTERU2008426//	0	//	0.000	//	26.260
35	UTERU2008516//	0	//	0.000	//	100.000
	UTERU2008561//	0	//	0.000	//	100.000

	UTERU2008653//	0	//	0.000	//	48.981
	UTERU2008705//	0	//	0.000	//	100.000
	UTERU2008707//	0	//	0.000	//	100.000
	UTERU2008747//	0	//	0.000	//	10.541
5	UTERU2008785//	0	//	0.000	//	100.000
	UTERU2008845//	0	//	0.000	//	100.000
	UTERU2008901//	0	//	0.000	//	100.000
	UTERU2008930//	0	//	0.000	//	100.000
	UTERU2008938//	0	//	0.000	//	8.806
10	UTERU2008939//	0	//	0.000	//	17.716
	UTERU2008962//	0	//	0.000	//	64.596
	UTERU2009094//	0	//	0.000	//	100.000
	UTERU2009120//	0	//	0.000	//	100.000
	UTERU2009131//	0	//	0.000	//	100.000
15	UTERU2009147//	0	//	0.000	//	100.000
	UTERU2009206//	0	//	0.000	//	100.000
	UTERU2009283//	0	//	0.000	//	100.000
	UTERU2009335//	0	//	0.000	//	10.852
	UTERU2009414//	0	//	0.000	//	100.000
20	UTERU2009435//	0	//	0.000	//	12.756
	UTERU2009483//	0	//	0.000	//	100.000
	UTERU2009510//	0	//	0.000	//	17.926
	UTERU2009538//	0	//	0.000	//	40.674
	UTERU2009540//	0	//	0.000	//	100.000
25	UTERU2009776//	0	//	0.000	//	100.000
	UTERU2009904//	0	//	0.000	//	100.000
	UTERU2009951//	0	//	0.000	//	100.000
	UTERU2009972//	0	//	0.000	//	16.901
	UTERU2010115//	0	//	0.000	//	100.000
30	UTERU2010124//	0	//	0.000	//	100.000
	UTERU2010164//	0	//	0.000	//	100.000
	UTERU2010226//	0	//	0.000	//	9.408
	UTERU2010231//	0	//	0.000	//	100.000
	UTERU2010304//	0	//	0.000	//	100.000
35	UTERU2010320//	0	//	0.000	//	25.187
	UTERU2010417//	7.026	//	0	//	1.128

	UTERU2010431// 0 // 0.000 // 100.000
	UTERU2010525// 0 // 0.000 // 14.053
	UTERU2010651// 0 // 0.000 // 100.000
	UTERU2010724// 0 // 0.000 // 100.000
5	UTERU2010747// 0 // 0.000 // 62.692
	UTERU2011195// 0 // 0.000 // 100.000
	UTERU2011199// 0 // 0.000 // 100.000
	UTERU2011220// 0 // 0.000 // 4.669
	UTERU2011261// 0 // 0.000 // 100.000
10	UTERU2011287// 0 // 0.000 // 39.146
	UTERU2011410// 0 // 0.000 // 100.000
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	UTERU2011657// 0 // 0.000 // 100.000
15	UTERU2011741// 0 // 0.000 // 14.051
	UTERU2011806// 0 // 0.000 // 49.807
	UTERU2011811// 0 // 0.000 // 100.000
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	UTERU2011906// 0 // 0.000 // 16.267
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	UTERU2012031// 0 // 0.000 // 53.896
	UTERU2012101// 0 // 0.000 // 100.000
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25	UTERU2012230// 0 // 0.000 // 18.890
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	UTERU2012333// 0 // 0.000 // 100.000
	UTERU2012407// 0 // 0.000 // 29.356
30	UTERU2012526// 0 // 0.000 // 11.013
	UTERU2012581// 0 // 0.000 // 100.000
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	UTERU2012615// 0 // 0.000 // 100.000
	UTERU2012688// 0 // 0.000 // 51.568
35	UTERU2012703// 0 // 0.000 // 24.539
	UTERU2012715// 0 // 0.000 // 34.205

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5	UTERU2012890//	0	//	0.000	//	100.000
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	UTERU2013078//	0	//	0.000	//	16.358
10	UTERU2013231//	0	//	0.000	//	100.000
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	UTERU2013280//	0	//	0.000	//	100.000
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	UTERU2013483//	0	//	0.000	//	100.000
15	UTERU2013491//	0	//	0.000	//	13.929
	UTERU2013502//	0	//	0.000	//	40.214
	UTERU2013586//	0	//	0.000	//	7.858
	UTERU2013926//	0	//	0.000	//	100.000
	UTERU2013976//	0	//	0.000	//	100.000
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	UTERU2014024//	0	//	0.000	//	15.457
	UTERU2014167//	0	//	0.000	//	1.087
	UTERU2014223//	0	//	0.000	//	100.000
	UTERU2014398//	0	//	0.000	//	100.000
25	UTERU2014464//	0	//	0.000	//	16.101
	UTERU2014548//	0	//	0.000	//	39.231
	UTERU2014601//	0	//	0.000	//	16.520
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	UTERU2014898//	0	//	0.000	//	1.815
	UTERU2014998//	0	//	0.000	//	100.000
	UTERU2015062//	0	//	0.000	//	17.070
35	UTERU2015087//	0	//	0.000	//	100.000
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	UTERU2015405// 0 // 0.000 // 100.000
5	UTERU2015640// 0 // 0.000 // 100.000
	UTERU2015653// 0 // 0.000 // 4.175
	UTERU2015830// 0 // 0.000 // 58.853
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10	UTERU2016157// 0 // 0.000 // 100.000
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	UTERU2016464// 0 // 0.000 // 100.000
	UTERU2016669// 0 // 0.000 // 9.848
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15	UTERU2016761// 0 // 0.000 // 100.000
	UTERU2016799// 0 // 0.000 // 10.404
	UTERU2016822// 0 // 0.000 // 19.178
	UTERU2016896// 0 // 0.000 // 100.000
	UTERU2016902// 0 // 0.000 // 100.000
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	UTERU2017421// 0 // 0.000 // 100.000
25	UTERU2017492// 0 // 0.000 // 5.197
	UTERU2017613// 0 // 0.000 // 12.264
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	UTERU2018333// 0 // 0.000 // 100.000

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10	UTERU2018784// 0 // 0.000 // 100.000
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	UTERU2018811// 0 // 0.000 // 100.000
	UTERU2018867// 0 // 0.000 // 100.000
	UTERU2018881// 0 // 0.000 // 100.000
15	UTERU2018884// 0 // 0.000 // 1.848
	UTERU2018955// 0 // 0.000 // 100.000
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	UTERU2019096// 0 // 0.000 // 5.495
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	UTERU2019710// 0 // 0.000 // 100.000
	UTERU2019940// 0 // 0.000 // 51.819
	UTERU2019959// 0 // 0.000 // 100.000
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	UTERU2020718// 0 // 0.000 // 100.000

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	UTERU2021820//	0	//	0.000	//	29.732
5	UTERU2022020//	0	//	0.000	//	100.000
	UTERU2022773//	0	//	0.000	//	100.000
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	UTERU2023039//	0	//	0.000	//	54.394
10	UTERU2023045//	0	//	0.000	//	10.794
	UTERU2023175//	0	//	0.000	//	7.103
	UTERU2023262//	0	//	0.000	//	15.042
	UTERU2023550//	0	//	0.000	//	9.988
	UTERU2023651//	0	//	0.000	//	29.963
15	UTERU2023687//	0	//	0.000	//	100.000
	UTERU2023712//	0	//	0.000	//	100.000
	UTERU2023941//	0	//	0.000	//	100.000
	UTERU2024002//	0	//	0.000	//	100.000
	UTERU2024042//	0	//	0.000	//	100.000
20	UTERU2024141//	0	//	0.000	//	100.000
	UTERU2024481//	0	//	0.000	//	100.000
	UTERU2024656//	0	//	0.000	//	51.568
	UTERU2024758//	0	//	0.000	//	100.000
	UTERU2024820//	0	//	0.000	//	100.000
25	UTERU2024881//	0	//	0.000	//	100.000
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	UTERU2025025//	0	//	0.000	//	100.000
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30	UTERU2025366//	0	//	0.000	//	100.000
	UTERU2025415//	0	//	0.000	//	100.000
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	UTERU2025645//	0	//	0.000	//	100.000
	UTERU2025891//	0	//	0.000	//	100.000
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5	UTERU2027369//	0	//	0.000	//	39.231
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10	UTERU2028734//	0	//	0.000	//	26.183
	UTERU2029503//	0	//	0.000	//	100.000
	UTERU2029660//	0	//	0.000	//	100.000
	UTERU2029742//	0	//	0.000	//	100.000
	UTERU2029953//	0	//	0.000	//	100.000
15	UTERU2030213//	0	//	0.000	//	58.763
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	UTERU2030280//	0	//	0.000	//	51.819
	UTERU2031060//	0	//	0.000	//	100.000
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20	UTERU2031268//	0	//	0.000	//	100.000
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	UTERU2031521//	0	//	0.000	//	100.000
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	UTERU2032075//	0	//	0.000	//	100.000
	UTERU2032220//	0	//	0.000	//	100.000
	UTERU2032279//	0	//	0.000	//	100.000
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	UTERU2033172//	0	//	0.000	//	100.000
	UTERU2033375//	0	//	0.000	//	1.385
	UTERU2033382//	0	//	0.000	//	100.000
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	UTERU2035114// 0 // 0.000 // 51.568
5	UTERU2035187// 0 // 0.000 // 100.000
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	UTERU3002600// 0 // 0.000 // 100.000
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	UTERU3002667// 0 // 0.000 // 100.000
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	UTERU3002731// 0 // 0.000 // 100.000
	UTERU3002768// 0 // 0.000 // 100.000
	UTERU3002786// 0 // 0.000 // 51.568
	UTERU3002993// 0 // 0.000 // 100.000
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5	UTERU3003660// 0 // 0.000 // 8.781
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	UTERU3005264// 0 // 0.000 // 100.000
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	UTERU3005460// 0 // 0.000 // 62.692
	UTERU3005536// 0 // 0.000 // 62.692
25	UTERU3005585// 0 // 0.000 // 100.000
	UTERU3005767// 26.525 // 0 // 7.098
	UTERU3005907// 0 // 0.000 // 15.610
	UTERU3005970// 0 // 0.000 // 62.692
	UTERU3006008// 0 // 0.000 // 100.000
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35	UTERU3006720// 0 // 0.000 // 100.000
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	UTERU3007108//	0	//	0.000	//	100.000
5	UTERU3007134//	0	//	0.000	//	100.000
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	UTERU3007913//	0	//	0.000	//	87.049
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Genes whose expression levels were negligibly low in each of the above-described libraries are shown with their clone names below.

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TRACH3032755, TRACH3032827, TRACH3032873, TRACH3033535,
TRACH3033680, TRACH3033868, TRACH3034145, TRACH3034414,
TRACH3034488, TRACH3034680, TRACH3034731, TRACH3034745,
25 TRACH3034762, TRACH3034903, TRACH3035187, TRACH3035199,
TRACH3035235, TRACH3035451, TRACH3035482, TRACH3035526,
TRACH3036004, TRACH3036103, TRACH3036193, TRACH3036207,
TRACH3036278, TRACH3036309, TRACH3036456, TRACH3036609,
TRACH3036638, TRACH3036683, TRACH3036750, TRACH3036792,
30 TRACH3036843, TRACH3036897, TRACH3036932, TRACH3036942,
TRACH3036997, TRACH3037063, TRACH3037067, TRACH3037267,
TRACH3037288, TRACH3037505, TRACH3037573, TRACH3037696,
TRACH3037897, TRACH3038086,
TRACH3038399, TSTOM1000135, TSTOM1000186, TSTOM2000139,
35 TSTOM2000235, TSTOM2000315, TSTOM2000442, TSTOM2000553,
TSTOM2000569, TSTOM2000588, TSTOM2001195, TSTOM2001274,

TSTOM2001571, TSTOM2001996, TSTOM2002265, TSTOM2002505,
TSTOM2002561, TSTOM2002611, TSTOM2002672, TSTOM2002682

Homology search data

5 Homology search data for full-length nucleotide sequences and the deduced amino acid sequences are shown below. The search results contain two types of length unit for the sequences compared: aa and bb.

10 Each piece of data is punctuated with a double slash mark (//) and shown in order: Sequence Name, Definition of hit data, P value, Length of sequence compared, Homology, and Accession Number of hit data. Sequences which did not show hit data in the homology search list only the Clone name.

3NB692002685// Homo sapiens sperm acrosomal protein mRNA, complete cds.//
15 7.3E-117// 227aa// 100%// AF047437
3NB692002806// Dihydropteridine reductase (EC 1.6.99.7) (HDHPR) (Quinoid dihydropteridine reductase).// 1.00E-105// 192aa// 78%// P09417
3NB692008729
ACTVT2000380
20 ADIPS2000088// Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementarity-determining regions mRNA, complete cds.//
3.5E-236// 477aa// 90%// M87789
ADRGL2000172
ADRGL2003329
25 ADRGL2009146
ADRGL2009691// Mus musculus D111gp1 mRNA, complete cds.// 5.1E-17// 75aa//
60%// AF316996
ADRGL2009755// Homo sapiens brain and reproductive organ-expressed protein (BRE) mRNA, complete cds.// 2.2E-156// 308aa// 93%// AF015767
30 ADRGL2012038
ADRGL2012179
ASTRO1000009// BAND 4.1-LIKE PROTEIN 4 (NBL4 PROTEIN).// 2.50E-45// 309aa//
38%// 057457
ASTRO2002842// sentrin/SUMO-specific protease [Mus musculus]// 2.00E-84//
35 148aa// 54%// NM_030702
ASTRO2003960

ASTR02014923// hypothetical protein // 2.6E-66// 133aa// 100%// CAB70760
 ASTR02018373
 ASTR03000172
 5 ASTR03000177// *Drosophila melanogaster* BcDNA. GH03694 (BcDNA. GH03694) mRNA,
 complete cds.// 1.30E-89// 385aa// 47%// AF181626
 ASTR03000301// G2 [*Homo sapiens*]// 0// 1073aa// 96%// AAA21253
 ASTR03000482
 BLADE1000176
 BLADE2001371
 10 BLADE2001987
 BLADE2002073
 BLADE2002782// *Rattus norvegicus* clone C53 CDK5 activator-binding protein
 mRNA, complete cds.// 1.90E-24// 70aa// 82%// AF177476
 BLADE2002947
 15 BLADE2003474
 BLADE2004089// *Mus musculus* PDZ domain actin binding protein Shroom mRNA,
 complete cds.// 4.20E-244// 784aa// 64%// AF199421
 BLADE2004462
 BLADE2004670
 20 BLADE2005036// CARBOXYPEPTIDASE A1 PRECURSOR (EC 3.4.17.1).// 1.20E-81//
 168aa// 93%// P15085
 BLADE2005459
 BLADE2007666
 BLADE2007958// *Homo sapiens* U5 snRNP-specific 40 kDa protein mRNA, complete
 25 cds// 6.0E-91// 190aa// 99%// NP_004805
 BLADE2008281
 BLADE2008398// *Homo sapiens* LRR FLI-1 interacting protein 2 (LRRFIP2) mRNA,
 complete cds.// 2.00E-98// 200aa// 99%// AF115509
 BLADE2008539// tumor antigen SLP-8p [*Homo sapiens*]// 0// 427aa// 95%//
 30 NM_016516
 BNGH42003570// *Mus musculus* mRNA for thrombospondin type 1 domain, complete
 cds.// 2.30E-44// 239aa// 39%// AB016768
 BNGH420077// VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.// 4.1E-40//
 242aa// 37%// Q00808
 35 BRACE1000186// g20 protein [*Homo sapiens*]// 3.00E-74// 138aa// 85%//
 NM_016210

- BRACE1000258
 BRACE1000533
 BRACE1000572
 BRACE2003639
- 5 BRACE2005457// PENDRIN.// 1.30E-61// 371aa// 35%// 043511
 BRACE2006319// Homo sapiens mRNA for Fln29, complete cds.// 3E-157// 283aa//
 99%// AB007447
 BRACE2008594// Human protein serine/threonine kinase stk2 mRNA, complete
 cds.// 1.90E-39// 190aa// 44%// L20321
- 10 BRACE2010489// Mus musculus nucleolar protein C7 mRNA, complete cds.// 1.70E-
 149// 391aa// 76%// AF324899
 BRACE2011747
 BRACE2014306// Chromaffin granule amine transporter (Vesicular amine
 transporter 1) (VAT1).// 1.00E-15// 80aa// 22%// P54219
- 15 BRACE2014475
 BRACE2014657
 BRACE2015058
 BRACE2015314
 BRACE2016981// Sarcolemmal-associated protein [Homo sapiens]// 7.00E-18//
 20 72aa// 29%// NM_007159
 BRACE2018762// Homer, neuronal immediate early gene, 3 [Homo sapiens]//
 1.00E-144// 267aa// 77%// NM_004838
 BRACE2024627
 BRACE2026836// Mus musculus mRNA for smoothelin L1, large isoform.// 8.00E-
 25 66// 220aa// 55%// AJ010305
 BRACE2027258// Homo sapiens E2a-Pbx1-associated protein (EB-1) mRNA, partial
 cds.// 5.80E-163// 302aa// 99%// AF145204
 BRACE2027970
 BRACE2028970
- 30 BRACE2029112// Homo sapiens mRNA for plexin-B1 plasma membrane receptor,
 splice variant R (plexin-B1/SEP gene)// 4.0E-99// 119aa// 62%// AJ011415
 BRACE2029849
 BRACE2030326// OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).// 1.40E-07//
 106aa// 33%// P18749
- 35 BRACE2030341// Homo sapiens protein kinase STK10 mRNA, partial cds.// 2.60E-
 66// 129aa// 100%// AF170723

BRACE2030884
 BRACE2031154
 BRACE2031389
 BRACE2031527
 5 BRACE2031531
 BRACE2031899
 BRACE2032044
 BRACE2032329
 BRACE2032385
 10 BRACE2032538
 BRACE2032823
 BRACE2033720
 BRACE2035381// Homo sapiens phospholipase A2, group IVB (cytosolic)
 (PLA2G4B), mRNA// 0// 446aa// 96%// NM_005090
 15 BRACE2035441
 BRACE2036005
 BRACE2036096
 BRACE2036830
 BRACE2036834
 20 BRACE2037847
 BRACE2038114
 BRACE2038329// Rattus norvegicus CBL-B (Cbl-b) mRNA, partial cds.// 3.4E-96//
 198aa// 92%// AF199504
 BRACE2038551// PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).// 6.40E-
 25 53// 102aa// 100%// P55345
 BRACE2039249// POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)
 (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-
 ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).// 5.1E-99// 199aa// 88%//
 Q10472
 30 BRACE2039327// hypothetical protein FLJ20241 // 6.3E-47// 97aa// 100%//
 XP_012789
 BRACE2039475
 BRACE2039734
 BRACE2040138
 35 BRACE2040325
 BRACE2041009

- BRACE2041200// PROTEIN-ARGININE DEIMINASE TYPE II (EC 3.5.3.15)
(PEPTIDYLARGININE DEIMINASE II) (KIAA0994).// 5.9E-98// 181aa// 98%// Q9Y2J8
BRACE2041264
BRACE2042550// Bos taurus mRNA for SCO-spondin, partial.// 1.8E-154// 319aa//
5 80%// AJ133488
BRACE2043142
BRACE2043248// Human I(3)mbt protein homolog mRNA, complete cds.// 7.1E-71//
140aa// 98%// U89358
BRACE2043349
10 BRACE2043665
BRACE2044286// GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER)
(MCF2 TRANSFORMING SEQUENCE-LIKE PROTEIN).// 7.20E-154// 578aa// 50%// Q64096
BRACE2044816
BRACE2044949
15 BRACE2045300// COFILIN, NON-MUSCLE ISOFORM.// 3.9E-85// 166aa// 100%// P23528
BRACE2045428
BRACE2045596// CTD-BINDING SR-LIKE PROTEIN RA4 (FRAGMENT).// 1.6E-08//
160aa// 32%// Q63627
BRACE2045772// 2-AMINO-3-KETOBUTYRATE COENZYME A LIGASE, MITOCHONDRIAL
20 PRECURSOR (EC 2.3.1.29) (AKB LIGASE) (GLYCINE ACETYLTRANSFERASE).// 1.3E-
107// 142aa// 98%// 075600
BRACE2045947
BRACE2045954
BRACE2046251// Homo sapiens hucep-10 mRNA for cerebral protein-10, complete
25 cds.// 4.3E-135// 264aa// 97%// AB000782
BRACE2046295// NTAK PROTEIN (NEURAL- AND THYMUS-DERIVED ACTIVATOR FOR ERBB
KINASES).// 1.80E-165// 304aa// 99%// 014511
BRACE2047011
BRACE2047350
30 BRACE2047377// ras inhibitor [Homo sapiens]// 4.40E-11// 60aa// 58%//
AAA36553
BRACE2047385
BRACE3000071
BRACE3000697
35 BRACE3000787

BRACE3000840// Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein).// 0// 979aa// 96%// Q13075
 BRACE3000973
 BRACE3001002// Zinc finger X-linked protein ZXDB.// 1.00E-45// 97aa// 70%//
 5 P98169
 BRACE3001217
 BRACE3001391// Polycystin precursor (Autosomal dominant polycystic kidney disease protein 1).// 0// 388aa// 84%// P98161
 BRACE3001595
 10 BRACE3001754// Surfeit locus protein 5.// 2.00E-87// 166aa// 83%// Q15528
 BRACE3002298
 BRACE3002390
 BRACE3002508// WD40 repeat domain 11 protein [Homo sapiens]// 1.00E-113//
 200aa// 98%// NM_018117
 15 BRACE3003004
 BRACE3003192// latent transforming growth factor beta binding protein 3 [Homo sapiens]// 0// 670aa// 91%// NM_021070
 BRACE3003595// CRK-associated substrate (p130Cas) (Breast cancer anti-estrogen resistance 1 protein).// 0// 712aa// 84%// P56945
 20 BRACE3003698
 BRACE3004058// NADH-cytochrome B5 reductase (EC 1.6.2.2) (B5R).// 1.00E-129//
 220aa// 96%// P00387
 BRACE3004113
 BRACE3004150// Heterogeneous nuclear ribonucleoprotein H (hnRNP H).// 0//
 25 390aa// 86%// P31943
 BRACE3004358
 BRACE3004435
 BRACE3004772// protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 [Homo sapiens]// 1.00E-101//
 30 168aa// 80%// NM_003625
 BRACE3004783
 BRACE3004843
 BRACE3004880
 BRACE3005145
 35 BRACE3005225
 BRACE3005430// DNA repair protein rad18.// 4.00E-21// 48aa// 38%// P53692

- BRACE3005499
 BRACE3006185
 BRACE3006226
 BRACE3006462
- 5 BRACE3006872// Echinoderm microtubule-associated protein-like 2 (EMAP-2)
 (HuEMAP-2).// 1.00E-46// 94aa// 34%// 095834
 BRACE3007322
 BRACE3007472
 BRACE3007480
- 10 BRACE3007559
 BRACE3007625// espin [Rattus norvegicus]// 1.00E-101// 178aa// 54%//
 NM_019622
 BRACE3007642
 BRACE3007767
- 15 BRACE3008036
 BRACE3008092
 BRACE3008137// Interleukin-16 precursor (IL-16) (Lymphocyte chemoattractant
 factor) (LCF).// 0// 530aa// 83%// Q14005
 BRACE3008384// rhomboid (veinlet, Drosophila)-like; Rhomboid, drosophila,
 20 homolog of [Homo sapiens]// 7.00E-94// 158aa// 51%// NM_003961
 BRACE3008720// SP00B-associated GTP-binding protein.// 5.00E-33// 80aa//
 43%// P20964
 BRACE3008772
 BRACE3009090
- 25 BRACE3009237
 BRACE3009297// mdgl-1 [Mus musculus]// 6.00E-54// 110aa// 84%// AAG17143
 BRACE3009377
 BRACE3009574
 BRACE3009701
- 30 BRACE3009708// Sodium/potassium-transporting ATPase alpha-2 chain precursor
 (EC 3.6.3.9) (Sodium pump 2) (Na⁺/K⁺ ATPase 2).// 0// 868aa// 98%// P50993
 BRACE3009724
 BRACE3009747// DAZ associated protein 1 [Homo sapiens]// 2.00E-18// 43aa//
 57%// NM_018959
- 35 BRACE3010397// Glioma pathogenesis-related protein (RTVP-1 protein).// 4.00E-
 29// 65aa// 37%// P48060

BRACE3010428

BRACE3011271// Patched protein homolog 1 (PTC1) (PTC).// 5.00E-84// 147aa//
72%// Q13635

BRACE3011421// Diacylglycerol kinase, zeta (EC 2.7.1.107) (Diglyceride
5 kinase) (DGK- zeta) (DAG kinase zeta).// 0// 839aa// 91%// Q13574

BRACE3011505

BRACE3012364

BRACE3012930

BRACE3013119

10 BRACE3013576

BRACE3013740

BRACE3013780

BRACE3014005// thymic stromal cotransporter; putative thymic stromal co-
transporter TSCOT [Mus musculus]// 4.00E-21// 71aa// 23%// NM_021053

15 BRACE3014068

BRACE3014231

BRACE3014317

BRACE3014807// homolog 1; tweety homolog [Homo sapiens]// 3.00E-38// 75aa//
46%// NM_020659

20 BRACE3015027// Ras GTPase-activating protein nGAP.// 3.00E-75// 214aa// 35%//
Q9UJF2

BRACE3015121

BRACE3015262// espin [Mus musculus]// 1.00E-10// 55aa// 40%// AAF98134

BRACE3015521// EH-domain containing protein 1 (Testilin) (hPAST1).// 1.00E-
25 121// 215aa// 93%// Q9H4M9

BRACE3015894

BRACE3016884// Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-
glucosidase) (1,4-alpha-D-glucan glucohydrolase).// 8.00E-07// 87aa// 17%//
P08640

30 BRACE3018308

BRACE3018963// Exostosin-like 3 (Putative tumour suppressor protein EXTL3)
(Multiple exostosis-like protein 3) (Hereditary multiple exostoses gene
isolog) (EXT-related protein 1).// 6.00E-39// 69aa// 98%// 043909

BRACE3019055

- BRACE3019084// protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Homo sapiens]// 1.00E-130// 226aa// 93%// NM_003626
- BRACE3020194
- 5 BRACE3020286
- BRACE3020594// cytokine receptor-like factor 2: cytokine receptor CRL2 precursor [Homo sapiens]// 1.00E-27// 53aa// 73%// NM_022148
- BRACE3022769
- BRACE3023912
- 10 BRACE3024073// hypothetical protein similar to small G proteins, especially RAP-2A [Homo sapiens]// 8.00E-36// 77aa// 48%// NM_021183
- BRACE3024659
- BRACE3024662
- BRACE3025153
- 15 BRACE3025457// testis-specific protein TSP-NY [Homo sapiens]// 0// 413aa// 97%// NM_032573
- BRACE3025531
- BRACE3025630// Alkaline serine exoprotease A precursor (EC 3.4.21.-).// 4.00E-18// 53aa// 33%// P16588
- 20 BRACE3026008
- BRACE3026075
- BRACE3026735
- BRACE3027242
- BRACE3027326// RAP1 GTPase activating protein 1 (RAP1GAP).// 1.00E-177// 331aa// 50%// P47736
- 25 BRACE3027478
- BRACE3030103
- BRACE3031838
- BRACE3032983
- 30 BRACE3040856// Golgi Transport; Got1p [Saccharomyces cerevisiae]// 2.00E-13// 100aa// 45%// NP_014020
- BRACE3045033// polyamine-modulated factor 1: polyamine modulated factor 1 [Homo sapiens]// 1.00E-41// 82aa// 100%// NM_007221
- BRALZ2011796
- 35 BRALZ2012183
- BRALZ2012848

BRALZ2014484

BRALZ2016085// MONOCARBOXYLATE TRANSPORTER 3 (MCT 3) (RETINAL EPITHELIAL
MEMBRANE PROTEIN).// 4.2E-49// 244aa// 33%// Q90632

BRALZ2016498// Homo sapiens FKSG76 (FKSG76) mRNA, complete cds.// 4.8E-65//
5 127aa// 99%// AF345564

BRALZ2017359// Homo sapiens RNA helicase HDB/DICE1 mRNA, partial cds.// 4.4E-
62// 318aa// 47%// AF141326

BRAMY2001473// Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete
cds.// 3.00E-115// 501aa// 44%// U87306

10 BRAMY2003008

BRAMY2004771// CHONDROADHERIN PRECURSOR (CARTILAGE LEUCINE-RICH PROTEIN) (38
KDA BONE PROTEIN).// 2.30E-36// 293aa// 34%// Q27972

BRAMY2005052// COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR PRECURSOR
(COXSACKIEVIRUS B- ADENOVIRUS RECEPTOR) (HCAR) (CVB3 BINDING PROTEIN).//

15 3.10E-37// 200aa// 35%// P78310

BRAMY2017528

BRAMY2019300// CHONDROADHERIN PRECURSOR (CARTILAGE LEUCINE-RICH PROTEIN) (38
KDA BONE PROTEIN).// 8.10E-32// 350aa// 28%// Q27972

BRAMY2019963

20 BRAMY2019985

BRAMY2020058

BRAMY2020270

BRAMY2021498// Mus musculus papilin mRNA, complete cds.// 3E-89// 546aa//
37%// AF314171

25 BRAMY2028856

BRAMY2028914

BRAMY2029602

BRAMY2030098

BRAMY2030109// Homo sapiens hucep-4 mRNA for cerebral protein-4, complete
cds.// 7.6E-83// 280aa// 55%// D88259

30

BRAMY2030702

BRAMY2030703

BRAMY2030799

BRAMY2031317// Mus musculus semaphorin cytoplasmic domain-associated protein
3A (Semcap3) mRNA, complete cds.// 2.6E-169// 682aa// 50%// AF127084

35

BRAMY2031377

BRAMY2031442
BRAMY2032014
BRAMY2032242
BRAMY2032317
5 BRAMY2033003// solute carrier family 22 (organic anion transporter), member
8 // 5.1E-25// 60aa// 100%// XP_006015
BRAMY2033116
BRAMY2033267// Rattus norvegicus mRNA for acetoacetyl-CoA synthetase,
complete// 1.7E-42// 148aa// 66%// AB026291
10 BRAMY2033594
BRAMY2034185
BRAMY2034920
BRAMY2034993
BRAMY2036387
15 BRAMY2036396
BRAMY2036567// GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER)
(MCF2 TRANSFORMING SEQUENCE-LIKE PROTEIN).// 5.3E-47// 113aa// 83%// Q64096
BRAMY2036699
BRAMY2036913
20 BRAMY2037823
BRAMY2038100
BRAMY2038484// Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.// 3.8E-
65// 194aa// 60%// AF099935
BRAMY2038846
25 BRAMY2038904// Homo sapiens mRNA for X-like 1 protein.// 2.7E-199// 738aa//
55%// AJ005821
BRAMY2039872// Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA,
complete cds.// 4.1E-43// 84aa// 98%// AF157028
BRAMY2040478
30 BRAMY2040592// Homo sapiens hucep-11 mRNA for cerebral protein-11, complete
cds.// 2.20E-101// 327aa// 64%// AB001596
BRAMY2041261
BRAMY2041378
BRAMY2041542
35 BRAMY2042612
BRAMY2042641

BRAMY2042760
 BRAMY2042918
 BRAMY2044078
 BRAMY2044246
 5 BRAMY2045036
 BRAMY2046478
 BRAMY2046742
 BRAMY2046989// Protein bimA.// 4.00E-07// 60aa// 20%// P17885
 BRAMY2047169
 10 BRAMY2047420
 BRAMY2047676
 BRAMY2047746// nasopharyngeal carcinoma susceptibility protein [Homo sapiens]// 3.00E-18// 50aa// 42%// NM_013275
 BRAMY2047751// REGULATOR OF G-PROTEIN SIGNALING 12 (RGS12).// 1.3E-178//
 15 336aa// 100%// 014924
 BRAMY2047765
 BRAMY2047884
 BRAMY3000206
 BRAMY3000213// Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete
 20 cds.// 5.7E-85// 167aa// 99%// U93871
 BRAMY3001401
 BRAMY3001794// Rattus norvegicus Circadian Oscillatory Protein (SCOP) (Scop)// 1.00E-117// 206aa// 59%// NM_021657
 BRAMY3002312
 25 BRAMY3002620
 BRAMY3002803// p21-activated protein kinase 6 [Homo sapiens]// 0// 598aa// 87%// NM_020168
 BRAMY3002805
 BRAMY3004224
 30 BRAMY3004672
 BRAMY3004900
 BRAMY3004919// Adenylate cyclase, type V (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase).// 0// 831aa// 91%// Q04400
 BRAMY3005091// Phosphatidylinositol 4-kinase alpha (EC 2.7.1.67) (PI4-kinase)
 35 (PtdIns-4-kinase) (PI4K-alpha).// 1.00E-111// 192aa// 100%// P42356

- BRAMY3005932// Diacylglycerol kinase, zeta (EC 2.7.1.107) (Diglyceride kinase) (DGK- zeta) (DAG kinase zeta) (DGK-IV) (104 kDa diacylglycerol kinase).// 1.00E-35// 71aa// 98%// 008560
- BRAMY3006297
- 5 BRAMY3007206
- BRAMY3007609// nuclear RNA export factor 2; TAP like protein 2 [Homo sapiens]// 2.00E-80// 155aa// 60%// NM_017809
- BRAMY3008466// kinesin family member 21A [Mus musculus]// 1.00E-167// 277aa// 94%// NM_016705
- 10 BRAMY3008505
- BRAMY3008650
- BRAMY3009811
- BRAMY3010411
- BRAMY4000095// ERBB-3 receptor protein-tyrosine kinase precursor (EC 2.7.1.112) (Tyrosine kinase-type cell surface receptor HER3).// 0// 469aa// 80%// P21860
- 15 BRAMY4000229// CORONIN 2A (WD-REPEAT PROTEIN 2) (IR10).// 2.40E-87// 167aa// 71%// Q92828
- BRAMY4000277// Alpha-1B-glycoprotein.// 1.00E-163// 276aa// 100%// P04217
- 20 BRASW1000053
- BRASW1000125
- BRAWH1000127// Mus musculus mRNA for thrombospondin type 1 domain, complete cds.// 8.30E-49// 204aa// 43%// AB016768
- BRAWH2001395// MYELIN BASIC PROTEIN (MBP).// 7.90E-26// 64aa// 90%// P02686
- 25 BRAWH2001671
- BRAWH2001940// H.sapiens gene from PAC 1026E2, partial.// 0// 640aa// 98%// AL035289
- BRAWH2001973
- BRAWH2002560// deleted in bladder cancer chromosome region candidate 1 [Homo sapiens].// 0// 770aa// 52%// NP_055433
- 30 BRAWH2002761
- BRAWH2005315// neuronal-STOP protein // 5.5E-119// 441aa// 56%// CAA75930
- BRAWH2007658// COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR HOMOLOG PRECURSOR (MCAR).// 8.80E-14// 366aa// 24%// P97792
- 35 BRAWH2010000// golgi autoantigen, golgin subfamily a, 3; golgin-160 [Homo sapiens]// 5.00E-15// 148aa// 23%// NM_005895

BRAWH2010084
 BRAWH2010536// paraneoplastic antigen MA1// 5.00E-18// 100aa// 42%//
 NP_006020
 BRAWH2012162// KE03 protein [Homo sapiens]// 2.00E-97// 330aa// 55%//
 5 AAC17109
 BRAWH2012326
 BRAWH2013294
 BRAWH2013871
 BRAWH2014414// Cadherin-4 precursor (Retinal-cadherin) (R-cadherin) (R-
 10 CAD).// 0// 761aa// 90%// P55283
 BRAWH2014645
 BRAWH2014662
 BRAWH2014876
 BRAWH2014954// Mus musculus neuronal IL-16 mRNA, complete cds.// 4.40E-271//
 15 604aa// 84%// AF175292
 BRAWH2016221// T-CELL RECEPTOR BETA CHAIN ANA 11.// 2.90E-07// 80aa// 46%//
 P06333
 BRAWH2016439
 BRAWH2016702
 20 BRAWH2016724// MAP2=HMW-MAP2 {alternatively spliced} [rats, brain, mRNA
 Partial, 267 nt].// 3.8E-24// 74aa// 77%// S81002
 BRAWH3000078// Mus musculus adult male tongue cDNA, RIKEN full-length
 enriched library, clone:2310010M24, full insert sequence.// 1.20E-29//
 111aa// 52%// AK009282
 25 BRAWH3000100// dedicator of cyto-kinesis 1 [Homo sapiens]// 1.00E-10// 67aa//
 20%// NM_001380
 BRAWH3000314
 BRAWH3000345
 BRAWH3000491// 40S ribosomal protein S12.// 5.00E-42// 90aa// 84%// P46405
 30 BRAWH3001326// 5-azacytidine resistance protein azr1.// 4.00E-27// 74aa//
 31%// Q09189
 BRAWH3001475
 BRAWH3001891
 BRAWH3002574// Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
 35 (Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
 (Millimolar-calpain).// 1.00E-84// 156aa// 91%// P17655

BRAWH3002600// cadherin 23; waltzer; otocadherin [Mus musculus]// 3.00E-30//
 139aa// 28%// NM_023370
 BRAWH3002819
 BRAWH3002821// synaptotagmin-like 2 [Mus musculus]// 0// 358aa// 78%//
 5 NM_031394
 BRAWH3003522
 BRAWH3003555
 BRAWH3003727
 BRAWH3003801
 10 BRAWH3003992
 BRAWH3004453
 BRAWH3004666
 BRAWH3005132
 BRAWH3005422
 15 BRAWH3005912// MIC1 protein.// 1.00E-29// 71aa// 28%// P53258
 BRAWH3005981
 BRAWH3006548
 BRAWH3006792
 BRAWH3007221
 20 BRAWH3007506
 BRAWH3007592
 BRAWH3007726
 BRAWH3007783
 BRAWH3008341// Ubiquitin carboxyl-terminal hydrolase 6 (EC 3.1.2.15)
 25 (Ubiquitin thiolesterase 6) (Ubiquitin-specific processing protease 6)
 (Deubiquitinating enzyme 6) (Proto-oncogene TRE-2).// 3.00E-63// 123aa//
 67%// P35125
 BRAWH3008634
 BRAWH3008697
 30 BRAWH3008931
 BRAWH3009297
 BRCAN2002562// Splicing factor, arginine/serine-rich 2 (Splicing factor SC35)
 (SC-35) (Splicing component, 35 kDa) (PR264 protein).// 6.00E-47// 88aa//
 88%// Q62093

- BRCAN2002856// AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY A MEMBER 2 (NEURON- SPECIFIC X11L PROTEIN) (NEURONAL MUNC18-1-INTERACTING PROTEIN 2) (MINT-2) (ADAPTER PROTEIN X11BETA).// 2.20E-89// 191aa// 93%// Q99767
- 5 BRCAN2002944// Mus musculus huntington yeast partner C (Hypc) mRNA, complete cds.// 2.1E-36// 83aa// 87%// AF135440
- BRCAN2002948// Homo sapiens mRNA for gamma2-adaptin, complete cds.// 6.6E-53// 117aa// 97%// AB015318
- BRCAN2003703// Homo sapiens mRNA for putative serine/threonine protein kinase, partial.// 1.4E-81// 187aa// 89%// AJ006701
- 10 BRCAN2003746// PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, SKELETAL MUSCLE ISOFORM (PHOSPHORYLASE KINASE ALPHA M SUBUNIT).// 5.9E-105// 213aa// 94%// P46020
- BRCAN2003987
- BRCAN2004355
- 15 BRCAN2005436
- BRCAN2006063// COCHLIN PRECURSOR (COCH-5B2).// 5.7E-123// 230aa// 100%// O43405
- BRCAN2006290
- BRCAN2006297
- 20 BRCAN2006450
- BRCAN2007144
- BRCAN2007409
- BRCAN2007426
- BRCAN2008528
- 25 BRCAN2009203// Homo sapiens liprin-alpha2 mRNA, complete cds.// 1.2E-235// 273aa// 93%// AF034799
- BRCAN2009432// hypothetical protein similar to small G proteins, especially RAP-2A [Homo sapiens]// 1.00E-93// 170aa// 92%// NM_021183
- BRCAN2010376
- 30 BRCAN2011254
- BRCAN2011602
- BRCAN2012355
- BRCAN2012481
- BRCAN2013655
- 35 BRCAN2013660// Arabidopsis thaliana putative protein (F4F15.330) mRNA, complete cds.// 1.1E-24// 138aa// 44%// AF370547

- BRCAN2014143
 BRCAN2014602// DIACYLGLYCEROL KINASE, ZETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK- ZETA) (DAG KINASE ZETA).// 6.5E-38// 74aa// 94%// Q13574
 BRCAN2014881
- 5 BRCAN2015371
 BRCAN2015464
 BRCAN2016433
 BRCAN2016619// CRK-associated substrate (p130Cas) (Breast cancer anti-estrogen resistance 1 protein).// 0// 735aa// 84%// P56945
- 10 BRCAN2017442// sarcosine dehydrogenase; dimethylglycine dehydrogenase-like 1. [Homo sapiens]// 5.00E-20// 51aa// 59%// NM_007101
 BRCAN2017717
 BRCAN2017905
 BRCAN2018935
- 15 BRCAN2019387
 BRCAN2020710
 BRCAN2021028
 BRCAN2024451// REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) (FRAGMENT).// 1.5E-131// 324aa// 83%// 043566
- 20 BRCAN2024563
 BRCAN2025712
 BRCAN2028355// Ca²⁺/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma-E// 3E-254// 479aa// 98%// JC5636
 BRCOC2000670
- 25 BRCOC2001505// MYELIN BASIC PROTEIN (MBP).// 8.50E-26// 64aa// 90%// P02686
 BRCOC2003213// Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine-tRNA ligase) (HisRS).// 0// 421aa// 95%// P12081
 BRCOC2007034
 BRCOC2014033
- 30 BRCOC2016525
 BRCOC2019934
 BRCOC2020142
 BRHIP2000691
 BRHIP2000819// Human mRNA for actin binding protein p57, complete cds.// 1.3E-48// 96aa// 100%// D44497
- 35 BRHIP2000826

BRHIP2000920

BRHIP2001074

BRHIP2001805// Homo sapiens TREK-1 potassium channel (KCNK2) mRNA, complete cds.// 1.8E-49// 134aa// 80%// AF129399

5 BRHIP2001927// Mus musculus mRNA for HS1 binding protein 3.// 2.7E-30// 102aa// 68%// AJ132192

BRHIP2002122// Homo sapiens B aggressive lymphoma long isoform (BAL) mRNA, complete cds.// 1.8E-97// 189aa// 100%// AF307338

10 BRHIP2002172// Mus musculus urea transporter isoform UTA-3 mRNA, complete cds.// 6.9E-208// 452aa// 82%// AF258602

BRHIP2002346

BRHIP2003242

BRHIP2003786// CCA3 [Rattus norvegicus]// 2.60E-199// 603aa// 61%// BAA19969

BRHIP2003917

15 BRHIP2004312

BRHIP2004359// ELAC PROTEIN.// 6.80E-20// 111aa// 37%// Q47012

BRHIP2004814// Homo sapiens gibbon ape leukemia virus receptor 1 (SLC20A1) gene, exon 11 and complete cds.// 1.8E-188// 346aa// 99%// AF102063

BRHIP2004883

20 BRHIP2005236// latrophilin 2 splice variant baaae // 1.3E-203// 250aa// 97%// AAD05305

BRHIP2005354

BRHIP2005600

BRHIP2005719

25 BRHIP2005752// NG5 [Homo sapiens]// 5.0E-61// 200aa// 100%// AAB47496

BRHIP2005932

BRHIP2006800

BRHIP2007616// plexin 2// 7.5E-137// 423aa// 59%// BAA13189

BRHIP2007741

30 BRHIP2009340

BRHIP2009414// Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).// 3.00E-97// 177aa// 77%// P55061

BRHIP2009474

BRHIP2013699

35 BRHIP2014228

BRHIP2021615// Homo sapiens CUG-BP and ETR-3 like factor 4 (CELF4) mRNA,
complete cds.// 9.60E-115// 349aa// 65%// AF329265
BRHIP2022221
BRHIP2024146
5 BRHIP2024165// Synthase [Homo sapiens]// 5.00E-44// 83aa// 94%// NM_003896
BRHIP2026061
BRHIP2026288// Protein bem46.// 2.00E-47// 110aa// 41%// P54069
BRHIP2029176
BRHIP2029393// COBW-like protein [Homo sapiens]// 3.00E-89// 158aa// 98%//
10 NM_018491
BRHIP3000339// MYELIN BASIC PROTEIN (MBP).// 8.5E-26// 64aa// 90%// P02686
BRHIP3000526
BRHIP3001283
BRHIP3006683
15 BRHIP3007483
BRHIP3007586
BRHIP3008183
BRHIP3008313// testis specific ankyrin-like protein 1 [Homo sapiens]// 1.00E-
120// 210aa// 92%// NM_016552
20 BRHIP3008344
BRHIP3008405// Dynamin 2 (EC 3.6.1.50) (Dynamin UDNM).// 1.00E-56// 108aa//
90%// P39054
BRHIP3008565
BRHIP3008598
25 BRHIP3008997
BRHIP3009099
BRHIP3009448// 2-19 protein precursor.// 1.00E-102// 179aa// 99%// P98173
BRHIP3011241
BRHIP3013765
30 BRHIP3013897
BRHIP3015751
BRHIP3016213
BRHIP3018797
BRHIP3020182
35 BRHIP3024118// Monocarboxylate transporter 4 (MCT 4) (MCT 3).// 1.00E-36//
108aa// 30%// 035910

BRHIP3024533

BRHIP3024725

BRHIP3025161// Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (Faciogenital dysplasia protein homolog).// 2.00E-75// 175aa// 30%//

5 P52734

BRHIP3025702

BRHIP3026097

BRHIP3027137// 10-formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) (10-FTHFDH).// 1.00E-119// 208aa// 93%// 075891

10 BRHIP3027854// Homo sapiens ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2)// 1.00E-130// 222aa// 94%// NM_006209

BRSSN2000684// CDC14 homolog B, isoform 3 [Homo sapiens]// 3.00E-12// 52aa// 30%// NM_033332

BRSSN2003086

15 BRSSN2004496// TASP for testis-specific adriamycin sensitivity protein [Homo sapiens]// 5.00E-45// 101aa// 39%// NM_018697

BRSSN2004719// SHC transforming protein.// 4.00E-39// 89aa// 53%// P29353

BRSSN2006892

20 BRSSN2008549// oxysterol binding protein 2 [Mus musculus]// 1.00E-149// 252aa// 75%// NM_024289

BRSSN2008797

BRSSN2011262

BRSSN2011738

BRSSN2013874// TEMO [Rattus norvegicus]// 2.00E-53// 99aa// 98%// NM_023986

25 BRSSN2014299// TPA inducible gene-1; TPA inducible protein [Homo sapiens]// 2.00E-47// 93aa// 86%// NM_015889

BRSSN2014424// transporter-like protein [Homo sapiens]// 0// 413aa// 92%// NM_022109

BRSSN2014556

30 BRSSN2018581

BRSSN2018925

BRSTN2000872// Protein disulfide isomerase A2 precursor (EC 5.3.4.1) (PDip).// 0// 341aa// 92%// Q130°7

BRSTN2001067

35 BRSTN2001613// HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP C2).// 2.8E-34// 214aa// 43%// P07910

BRSTN2002400
BRSTN2003835
BRSTN2004863// *Drosophila melanogaster* polypeptide N-acetylgalactosaminyltransferase mRNA, complete cds.// 5.60E-126// 526aa//
5 47%// AF158747
BRSTN2004987// *Homo sapiens* mRNA for mitochondrial tryptophanyl-tRNA synthetase (WARS2 gene).// 1.20E-162// 360aa// 86%// AJ242739
BRSTN2005721
BRSTN2006865
10 BRSTN2007000
BRSTN2007284
BRSTN2008052
BRSTN2008283
BRSTN2008418// Breakpoint cluster region protein (EC 2.7.1.-).// 7.00E-33//
15 70aa// 75%// P11274
BRSTN2008457
BRSTN2009899
BRSTN2010363
BRSTN2010500
20 BRSTN2010750
BRSTN2012320
BRSTN2012380
BRSTN2013741// Ras-related protein M-Ras (Ras-related protein R-Ras3).//
1.00E-105// 189aa// 90%// 014807
25 BRSTN2015015
BRSTN2016470
BRSTN2016678
BRSTN2017084
BRSTN2017110
30 BRSTN2017237
BRSTN2017771// *Homo sapiens* putative BTK-binding protein mRNA, complete cds.// 1.0E-41// 90aa// 99%// AF235049
BRSTN2018083
BRSTN2019129
35 BRTHA1000311
BRTHA2000855

BRTHA2001462
 BRTHA2002115
 BRTHA2002281// Rho guanine nucleotide exchange factor 10 [Homo sapiens].//
 5.0E-26// 123aa// 39%// NP_055444.1
 5 BRTHA2002376
 BRTHA2002442
 BRTHA2002493
 BRTHA2002608// aldehyde dehydrogenase 1A3// 2.00E-19// 46aa// 88%// NP_000684
 BRTHA2002808// GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR.// 7.8E-
 10 65// 141aa// 90%// P13284
 BRTHA2003030
 BRTHA2003110// Protein Clorf8 precursor (Liver membrane-bound protein)
 (HSPC001).// 1.00E-98// 178aa// 92%// Q9BXS4
 BRTHA2003116
 15 BRTHA2003461
 BRTHA2004821
 BRTHA2004978
 BRTHA2005579// Xenopus laevis mRNA for Kielin, complete cds.// 1.3E-190//
 659aa// 47%// AB026192
 20 BRTHA2005956
 BRTHA2006075
 BRTHA2006146
 BRTHA2006194
 BRTHA2007122// ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN,
 25 NONERYTHROID).// 6.1E-18// 203aa// 32%// Q01484
 BRTHA2007422
 BRTHA2007603// H. sapiens mRNA for BCL7B protein.// 1.8E-56// 116aa// 98%//
 X89985
 BRTHA2008316
 30 BRTHA2008335
 BRTHA2008527// LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-
 R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR).// 7.5E-66// 189aa// 73%// P22888
 BRTHA2008535
 BRTHA2008955
 35 BRTHA2009311// EOSINOPHIL LYSOPHOSPHOLIPASE// 1.0E-30// 64aa// 91%// P97400
 BRTHA2009846

BRTHA2009972
BRTHA2010073
BRTHA2010608
BRTHA2010884
5 BRTHA2010907
BRTHA2011194
BRTHA2011351
BRTHA2011500
BRTHA2011641
10 BRTHA2012392// Homo sapiens HCDI (HCDI) mRNA, complete cds.// 8.0E-95//
194aa// 95%// AF226050
BRTHA2012562
BRTHA2012980// INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-
1) (IL-13RA-1).// 1.5E-44// 91aa// 100%// P78552
15 BRTHA2013262
BRTHA2013460
BRTHA2013707
BRTHA2014792// ENHANCER OF ZESTE HOMOLOG 1 (ENX-2) (KIAA0388).// 7.1E-21//
184aa// 35%// Q92800
20 BRTHA2014828
BRTHA2015406// Homo sapiens mRNA for putative serine/threonine protein kinase,
partial.// 1.90E-86// 268aa// 67%// AJ006701
BRTHA2015478
BRTHA2015696
25 BRTHA2015878
BRTHA2016215
BRTHA2016496// Vacuolar processing enzyme precursor (EC 3.4.22.-) (VPE).//
0// 370aa// 79%// P49043
BRTHA2016543
30 BRTHA2017353
BRTHA2017985
BRTHA2018165
BRTHA2018344
BRTHA2018591
35 BRTHA2018624// Oncorhynchus mykiss stl3 mRNA for rhamnose binding lectin STL3,
complete cds.// 7.40E-21// 167aa// 34%// AB039024

BRTHA2018707
 BRTHA2019014
 BRTHA2019022
 BRTHA2019048
 5 BRTHA3000273
 BRTHA3000297
 BRTHA3000633// single-pass transmembrane protein [Rattus norvegicus]// 5.00E-48// 220aa// 54%// BAA90767
 BRTHA3001721// TATA box binding protein (TBP)-associated factor, RNA
 10 polymerase III, GTF3B subunit 2; TATA box binding protein (TBP)-associated factor, RNA polymerase III, C, 90kD; general transcription factor IIIB, 90kD [Homo sapiens]// 4.00E-71// 135aa// 85%// NM_001519
 BRTHA3002401
 BRTHA3002427// Sodium- and chloride-dependent betaine transporter (Na⁺/Cl⁻-betaine/GABA transporter) (BGT-1).// 0// 553aa// 96%// P48065
 15 BRTHA3002933// uroplakin 3 [Homo sapiens]// 1.00E-158// 260aa// 99%// XP_001216
 BRTHA3003074// putative prostate cancer susceptibility protein; hypothetical protein FLJ10530 [Homo sapiens]// 0// 435aa// 94%// NM_018127
 20 BRTHA3003343// DAZ associated protein 1 [Homo sapiens]// 1.00E-95// 223aa// 92%// NP_061832
 BRTHA3003449// MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).// 4.70E-215// 400aa// 100%// P35749
 BRTHA3003474
 25 BRTHA3003490
 BRTHA3004475
 BRTHA3005046
 BRTHA3006856
 BRTHA3007113
 30 BRTHA3007148
 BRTHA3007319
 BRTHA3007769
 BRTHA3008143
 BRTHA3008310// Mus musculus mRNA for iroquois homeobox protein 6 (Irx6 gene).// 1.20E-176// 444aa// 76%// AJ271055
 35 BRTHA3008386

- BRTHA3008520// sporulation-induced transcript 4-associated protein;
hypothetical protein FLJ11058 [Homo sapiens]// 1.00E-164// 287aa// 87%//
NM_018312
- 5 BRTHA3008778// Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate—CoA
ligase) (Acyl- activating enzyme).// 1.00E-168// 286aa// 51%// 068040
BRTHA3009037// Regulator of G-protein signaling 3 (RGS3) (RGP3).// 0//
479aa// 92%// P49796
- BRTHA3009090// neuropathy target esterase [Homo sapiens]// 0// 784aa// 60%//
NM_006702
- 10 BRTHA3009291
BRTHA3010366
BRTHA3013884// Sorting nexin 14 (Fragment).// 0// 359aa// 95%// Q9Y5W7
BRTHA3015815// Selenide, water dikinase 1 (EC 2.7.9.3) (Selenophosphate
synthetase 1) (Selenium donor protein 1).// 1.00E-159// 275aa// 99%// P49903
- 15 BRTHA3015910
BRTHA3016845
BRTHA3016917// Valyl-tRNA synthetase 2 (EC 6.1.1.9) (Valine—tRNA ligase 2)
(VALRS 2).// 4.00E-82// 169aa// 43%// P26640
BRTHA3017047
- 20 BRTHA3017589// junctional adhesion molecule 3 [Homo sapiens]// 1.00E-119//
213aa// 74%// NM_031470
BRTHA3017848// Organic cation/carnitine transporter 2 (Solute carrier family
22, member 5) (High-affinity sodium-dependent carnitine cotransporter).//
2.00E-42// 105aa// 35%// 076082
- 25 BRTHA3018514
BRTHA3018617
BRTHA3018656
BRTHA3019105
CERVX1000042
- 30 CERVX2002006
COLON1000030
COLON2000470// Rattus norvegicus nucleolar protein C7C mRNA, complete cds.//
5.9E-51// 187aa// 49%// AF333986
COLON2000568// Ig alpha-2 chain C region.// 0// 324aa// 95%// P01877
- 35 COLON2001721// GLUT4 vesicle protein [Mus musculus]// 8.00E-36// 160aa//
39%// AAD10190

- COLON2002443
COLON2002520// Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).// 0// 447aa// 70%// Q27991
- 5 COLON2003043
COLON2004478// protein Tro alpha1 H, myeloma // 3.2E-233// 475aa// 88%// 0501254A
COLON2005126
COLON2005772// Homo sapiens candidate taste receptor T2R14 gene, complete
- 10 cds.// 3.9E-54// 112aa// 97%// AF227138
COLON2006282
COLON2009499
CORDB1000140
CORDB2000061
- 15 CORDB2000541// F-actin capping protein beta subunit (CAPZ beta).// 1.00E-126// 217aa// 99%// P79136
CTONG1000087
CTONG1000088
CTONG1000288
- 20 CTONG1000302
CTONG1000341// THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN).// 1.0E-283// 488aa// 99%// P07204
CTONG1000467// Mus musculus mRNA for Deltex3, complete cds.// 5.00E-54// 203aa// 52%// AB015425
- 25 CTONG1000488
CTONG1000508
CTONG1000540
CTONG2000042// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M).// 2E-132// 841aa// 35%// P01023
- 30 CTONG2001877
CTONG2004062// ATPase subunit 6 [Homo sapiens].// 3.00E-71// 226aa// 91%// BAA07295
CTONG2006798// putative serine/threonine protein kinase [Schizosaccharomyces pombe]// 5.80E-69// 581aa// 27%// CAB66438
- 35 CTONG2008233// Bos taurus DnaJ1 protein mRNA, complete cds.// 0// 1376bp// 85%// AF308815

CTONG2009423// 5-HYDROXYTRYPTAMINE 7 RECEPTOR (5-HT-7) (5-HT-X) (SEROTONIN RECEPTOR) (5HT7).// 2.40E-44// 113aa// 78%// P34969

CTONG2009531

CTONG2010803// Regulator of G-protein signaling 3 (RGS3) (RGP3).// 0//

5 323aa// 92%// P49796

CTONG2013178// Homo sapiens serine protease DESC1 (DESC1) mRNA, complete cds.// 2E-90// 421aa// 43%// AF064819

CTONG2017500// Homo sapiens muscle disease-related protein mRNA, complete cds.// 1.30E-59// 239aa// 47%// AF204674

10 CTONG2019248

CTONG2019652

CTONG2019704

CTONG2019788

CTONG2019833

15 CTONG2020026// Drosophila melanogaster BcDNA. GH09358 (BcDNA. GH09358) mRNA, complete cds.// 4.2E-187// 669aa// 45%// AF181639

CTONG2020127

CTONG2020522

CTONG2020638

20 CTONG2020806

CTONG2021132

CTONG2022153

CTONG2022601

CTONG2023021// H.sapiens mRNA for TFG protein.// 2.3E-88// 160aa// 100%//

25 Y07968

CTONG2023512// Homo sapiens PIG-T mRNA for phosphatidyl inositol glycan class T, complete cds.// 7.1E-158// 289aa// 100%// AB057724

CTONG2024206

CTONG2024749// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M).// 1.1E-174//

30 699aa// 46%// P06238

CTONG2025496// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M).// 1.2E-218//

977aa// 45%// P01023

CTONG2025516// general transcription factor II, i, isoform 3; BTK-associated protein, 135kD; Williams-Beuren syndrome chromosome region 6; Bruton tyrosine

35 kinase-associated protein 135; TFII-I protein; SPIN protein [Homo sapiens]//

2.00E-28// 57aa// 89%// NM_033001

CTONG2025900
CTONG2026920
CTONG2027327
CTONG2028124// very long-chain acyl-CoA synthetase homolog 1: VLCS-H1 protein
5 [Homo sapiens]// 5.00E-86// 156aa// 48%// NM_014031
CTONG2028687
CTONG3000084// PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE
TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE).// 4.3E-276//
519aa// 100%// Q12774
10 CTONG3000657
CTONG3000686
CTONG3000707
CTONG3000896
CTONG3001123// Mus musculus Pax transcription activation domain interacting
15 protein PTIP mRNA, complete cds.// 0// 965aa// 84%// AF104261
CTONG3001370// ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M).// 1.5E-267//
1008aa// 38%// Q61838
CTONG3001420
CTONG3001560
20 CTONG3002020
CTONG3002127// granuphilin [Mus musculus]// 1.00E-104// 204aa// 49%//
NM_013757
CTONG3002412// Human DOCK180 protein mRNA, complete cds.// 4.5E-236// 678aa//
66%// D50857
25 CTONG3002674
CTONG3003179
CTONG3003483
CTONG3003652
CTONG3003654
30 CTONG3003737// PLATELET GLYCOPROTEIN V PRECURSOR (GPV) (CD42D).// 1.80E-73//
434aa// 37%// 008770
CTONG3003905
CTONG3003972
CTONG3004072// GL002 protein [Homo sapiens]// 3.00E-80// 152aa// 88%//
35 NM_020193
CTONG3004712

CTONG3005325
 CTONG3005648
 CTONG3005713
 CTONG3005813
 5 CTONG3006067
 CTONG3006186// syntaxin binding protein 4 [Mus musculus]// 0// 427aa// 76%//
 NM_011505
 CTONG3006650
 CTONG3007444
 10 CTONG3007528
 CTONG3007586
 CTONG3007870
 CTONG3008252
 CTONG3008258// Homo sapiens GROS1-L protein mRNA, complete cds.// 7.70E-177//
 15 680aa// 51%// AF097432
 CTONG3008496
 CTONG3008566
 CTONG3008639// Human non-lens beta gamma-crystallin like protein (AIM1) mRNA,
 partial cds.// 0// 836aa// 99%// U83115
 20 CTONG3008831// Rattus norvegicus PGC1 mRNA for PPAR gamma coactivator,
 complete cds.// 2.9E-69// 176aa// 46%// AB025784
 CTONG3008894// Mus musculus SH3-domain binding protein 5// 3.00E-42// 89aa//
 40%// NM_011894
 CTONG3008951
 25 CTONG3009028// sno gene product [Drosophila melanogaster]// 1.00E-148//
 1000aa// 46%// AAF48240
 CTONG3009227
 CTONG3009239
 CTONG3009328
 30 CTONG3009385// Homo sapiens ARG99 mRNA, complete cds.// 2.4E-77// 153aa//
 100%// AF319520
 D30ST2002182// Homo sapiens mRNA for acetylglucosaminyltransferase-like
 protein.// 6.50E-11// 265aa// 23%// AJ007583
 D30ST2002648// PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR17 (R12).// 3E-24//
 35 184aa// 28%// Q13304

- D30ST3000169// Homo sapiens SH3-SAM adaptor protein (HACS1) mRNA, complete cds. // 2.40E-189// 354aa// 99%// AF218085
- DFNES1000107
- DFNES2000146// Mus musculus mRNA for thrombospondin type 1 domain, complete cds. // 4.10E-31// 135aa// 41%// AB016768
- 5 DFNES2001108// Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds. // 4.5E-41// 134aa// 63%// U93181
- DFNES2005266// ADAM-TS 1 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1). //
- 10 4.80E-15// 118aa// 30%// P97857
- DFNES2010502
- DFNES2011239
- DFNES2011499
- ERLTF2000324
- 15 FCBBF1000297// Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds. // 7.5E-186// 359aa// 99%// U28831
- FCBBF2001183
- FCBBF2007510
- FCBBF3001977
- 20 FCBBF3002163// chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated protein 1; KIAA0159 gene product [Homo sapiens]// 0// 840aa// 97%// NM_014865
- FCBBF3003435
- FCBBF3004502
- 25 FCBBF3004847
- FCBBF3006171
- FCBBF3007242
- FCBBF3007540// GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER)//
- 5.00E-46// 300aa// 38%// 015068
- 30 FCBBF3008944
- FCBBF3009888// Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds. // 5.30E-06// 122aa// 32%// AF043498
- FCBBF3012170// Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds. // 1.00E-80// 325aa// 51%// U72634
- 35 FCBBF3012288

FCBBF3013307// Homo sapiens RNA helicase-related protein mRNA, complete
cds.// 0// 644aa// 99%// AF083255

FCBBF3013846

FCBBF3021576

5 FCBBF3021940// SYNAPSIN I (FRAGMENT).// 5.00E-06// 128aa// 35%// 062732

FCBBF3023443

FCBBF3023895// contains simiarity to tubulin-tyrosine ligase [Caenorhabditis
elegans].// 1.00E-54// 220aa// 39%// AAF39893

FCBBF3025730

10 FCBBF3027717

FCBBF4000076

FEBRA1000030// T-CELL RECEPTOR BETA CHAIN ANA 11.// 2.7E-11// 131aa// 38%//
P06333

FEBRA2000253

15 FEBRA2006396

FEBRA2007544// transcription factor [Homo sapiens]// 0// 400aa// 99%//
AAG33674

FEBRA2007708// DRA PROTEIN (DOWN-REGULATED IN ADENOMA).// 2.60E-72// 511aa//
34%// P40879

20 FEBRA2007793

FEBRA2007801// Homo sapiens TRIAD3 mRNA, partial cds.// 2.3E-207// 358aa//
99%// AF228527

FEBRA2008287

FEBRA2008311// GALANIN RECEPTOR TYPE 1 (GAL1-R) (GALR1).// 1E-23// 299aa//
25 27%// P56479

FEBRA2008360

FEBRA2008468// LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR
(EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE)
(LIPASE A) (CHOLESTERYL ESTERASE).// 1.20E-179// 330aa// 97%// P38571

30 FEBRA2010719

FEBRA2014213

FEBRA2015588

FEBRA2020484

FEBRA2020582

35 FEBRA2020668

FEBRA2020886

FEBRA2021339
 FEBRA2021571
 FEBRA2021908
 FEBRA2021966
 5 FEBRA2024136
 FEBRA2024150
 FEBRA2024343
 FEBRA2024744// Homo sapiens Cat Eye Syndrome critical region protein isoform
 1 mRNA, complete cds.// 1.3E-126// 252aa// 94%// AF273270
 10 FEBRA2025427
 FEBRA2026984// TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSYL—TRNA LIGASE)
 (TYRRS) (FRAGMENT).// 7.80E-271// 528aa// 94%// Q29465
 FEBRA2027082
 FEBRA2027297
 15 FEBRA2027352
 FEBRA2028366
 FEBRA2028477
 FEBRA2028618
 HCASM2001301// MITOGEN-ACTIVATED PROTEIN KINASE 12 (EC 2.7.1.-)
 20 (EXTRACELLULAR SIGNAL-REGULATED KINASE 6) (EC 2.7.1.-) (ERK6) (ERK5) (STRESS-
 ACTIVATED PROTEIN KINASE-3) (MITOGEN-ACTIVATED PROTEIN KINASE P38 GAMMA) (MAP
 KINASE P38 GAMMA).// 2.2E-52// 104aa// 100%// P53778
 HCASM2002502
 HCASM2002918
 25 HCASM2003212
 HCASM2003415
 HCASM2007047
 HCASM2007737// SEC14-LIKE PROTEIN 1.// 8.30E-09// 162aa// 24%// Q92503
 HCHON2000028// Homo sapiens 7h3 protein mRNA, partial cds.// 2.1E-94//
 30 228aa// 82%// AF209931
 HCHON2000212
 HCHON2000244
 HCHON2000418
 HCHON2000626// X-linked protein STS1769.// 2.00E-47// 89aa// 83%// Q99871
 35 HCHON2001084// ARABINOSE-PROTON SYMPORTER (ARABINOSE TRANSPORTER).// 3E-66//
 321aa// 36%// P09830

- HCHON2001217// Homo sapiens cullin CUL4B (CUL4B) mRNA, complete cds.// 0//
782aa// 99%// AF212995
- HCHON2001548
- HCHON2001577// Human elastin gene, exon 1.// 1.5E-265// 585aa// 88%// M17282
- 5 HCHON2001712// Neutral amino acid transporter B(0) (ATB(0)).// 0// 369aa//
85%// Q15758
- HCHON2002676// ALPHA-L-IDURONIDASE PRECURSOR (EC 3.2.1.76).// 3.20E-274//
330aa// 99%// P35475
- HCHON2003532// PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE
10 KINASE BETA SUBUNIT).// 2.0E-159// 312aa// 95%// Q93100
- HCHON2004007// Potential phospholipid-transporting ATPase 1K (EC 3.6.3.13)
(Fragment).// 1.00E-160// 273aa// 93%// O60423
- HCHON2004531// UV excision repair protein RAD23 homolog B (HHR23B) (XP-C
repair complementing complex 58 kDa protein) (P58).// 1.00E-142// 270aa//
15 66%// P54727
- HCHON2004776// transmembrane protein (63kD), endoplasmic reticulum/Golgi
intermediate compartment [Homo sapiens]// 0// 500aa// 86%// NP_006816
- HCHON2005921// lipoma HMGIC fusion partner [Homo sapiens]// 1.00E-15// 52aa//
25%// NM_005780
- 20 HCHON2006250// Mus musculus SETA binding protein 1 (Sb1) mRNA, complete
cds.// 3.9E-269// 544aa// 91%// AF246218
- HCHON2006714
- HCHON2007881
- HCHON2008112// Homo sapiens HERC2 (HERC2) mRNA, complete cds.// 1.80E-24//
25 79aa// 70%// AF071172
- HCHON2008444// 28S ribosomal protein S15, mitochondrial precursor (MPR-S15)
(DC37).// 5.00E-39// 76aa// 76%// P82914
- HEART1000010// Hepatocyte growth factor-like protein precursor (Macrophage
stimulatory protein) (MSP) (Macrophage stimulating protein).// 5.00E-18//
30 40aa// 93%// P26927
- HEART1000074// BANP homolog; putative transcription factor; Btg3 associated
nuclear protein [Mus musculus]// 0// 420aa// 82%// NM_016812
- HEART1000088
- HEART1000139// TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).// 1.40E-112//
35 221aa// 98%// P45379
- HEART2001680// Ig alpha-1 chain C region.// 0// 324aa// 91%// P01876

- HEART2001756
 HEART2006131// 2-hydroxyphytanoyl-CoA lyase [*Mus musculus*]// 1.00E-138//
 263aa// 45%// NM_019975
 HEART2006909// Hemolysin C.// 3.00E-40// 88aa// 33%// Q54318
- 5 HEART2007031
 HEART2010391
 HEART2010492// GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
 (EC 2.3.1.15) (GPAT) (P90).// 3.6E-47// 462aa// 32%// Q61586
 HEART2010495// MICROTUBULE-ASSOCIATED PROTEIN 4.// 2.00E-159// 579aa// 62%//
- 10 P27816
 HHDPG1000118// Threonine synthase (EC 4.2.99.2).// 3.00E-70// 178aa// 35%//
 Q9ZMX5
 HHDPG2001337
 HLUNG1000017
- 15 HLUNG2000014// *Mus musculus* strain BALB/c dectin-2 alpha isoform mRNA,
 complete cds.// 2.80E-55// 211aa// 50%// AF240357
 HLUNG2001996
 HLUNG2002465// *Homo sapiens* Asef mRNA for APC-stimulated guanine nucleotide
 exchange factor, complete cds.// 1.30E-183// 557aa// 62%// AB042199
- 20 HLUNG2002958
 HLUNG2003003
 HLUNG2003872
 HLUNG2010464
 HLUNG2011041// basic proline-rich peptide IB-8a - human (fragments)// 9.7E-
- 25 07// 113aa// 35%// D38355
 HLUNG2011298// *Homo sapiens* cytochrome b5 reductase 1 (B5R.1) mRNA, complete
 cds.// 1.6E-27// 79aa// 78%// AF169481
 HLUNG2012049
 HLUNG2012287
- 30 HLUNG2012727
 HLUNG2013204// phytoene dehydrogenase-like [*Arabidopsis thaliana*]// 4.0E-53//
 97aa// 55%// BAB10768
 HLUNG2013304
 HLUNG2013622
- 35 HLUNG2013851
 HLUNG2014262

- HLUNG2014288// Mus musculus RP42 mRNA, complete cds.// 2.4E-40// 189aa// 43%// AF198092
- HLUNG2014449
- HLUNG2015617
- 5 HLUNG2017350// GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).// 2.60E-53// 262aa// 41%// P41987
- HLUNG2017546
- HLUNG2017806
- HLUNG2019058
- 10 HSYRA2004858
- HSYRA2005456
- HSYRA2005496// ENDOGLIN PRECURSOR (CD105 ANTIGEN).// 2.4E-117// 245aa// 92%// P17813
- HSYRA2006873
- 15 HSYRA2007667
- HSYRA2008376
- HSYRA2008714// POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE ID (EC 3.6.1.-) (FRAGMENT).// 6.2E-158// 412aa// 70%// P98198
- HSYRA2009075
- 20 HSYRA2009102// UDP-galactose transporter related [Homo sapiens].// 3.0E-26// 280aa// 32%// NP_005818
- IMR322000127// ZINC FINGER PROTEIN 135.// 3.30E-130// 426aa// 50%// P52742
- IMR322000917// ZINC FINGER PROTEIN 29 (ZFP-29).// 1.50E-34// 197aa// 40%// Q07230
- 25 IMR322001380// Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.// 7.00E-21// 216aa// 32%// AF186273
- IMR322002035
- IMR322002110
- IMR322003675
- 30 IMR322006222
- IMR322006495// Homo sapiens mRNA for kinetochore protein CENP-H, complete cds.// 3.1E-61// 183aa// 73%// AB035124
- IMR322006886// Homo sapiens hepatocellular carcinoma-associated antigen 127 (HCA127) mRNA, complete cds.// 2.5E-107// 207aa// 99%// AF270491
- 35 IMR322007225
- IMR322016146

IMR322018117
 KIDNE1000064// Mus musculus mRNA for RST, complete cds.// 6.70E-219// 552aa//
 73%// AB005451
 KIDNE2000665
 5 KIDNE2000722
 KIDNE2000832
 KIDNE2000846// Mus musculus orphan transporter isoform A12 (Xtrp2) mRNA,
 alternatively spliced, complete cds.// 1.2E-54// 203aa// 50%// AF075262
 KIDNE2001361// Mus musculus catp mRNA for cation-transporting atpase,
 10 complete cds.// 4.1E-123// 273aa// 91%// AB035381
 KIDNE2001847// H.sapiens graf gene.// 4.10E-98// 300aa// 55%// Y10388
 KIDNE2002252// Drosophila melanogaster BcDNA. GH09358 (BcDNA. GH09358) mRNA,
 complete cds.// 6.30E-145// 763aa// 42%// AF181639
 KIDNE2002991
 15 KIDNE2003837
 KIDNE2005543
 KIDNE2006580// CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1).// 1.10E-119//
 496aa// 49%// P29981
 KIDNE2010264
 20 KIDNE2011314
 KIDNE2011532// similar to melanoma-associated chondroitin sulfate
 proteoglycan 4// 7.00E-30// 54aa// 60%// XP_000655
 KIDNE2011635// Rabbit mRNA for sodium-glucose cotransporter, complete cds.//
 2.1e-313// 670aa// 80%// D16226
 25 KIDNE2012945// PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR (PCPE)
 (TYPE I PROCOLLAGEN COOH-TERMINAL PROTEINASE ENHANCER) (TYPE 1 PROCOLLAGEN C-
 PROTEINASE ENHANCER PROTEIN).// 2.00E-14// 113aa// 41%// Q15113
 KIDNE2013095
 LIVER2007415
 30 LYMPB1000141
 LYMPB2000083// HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F
 PRECURSOR (HLA F ANTIGEN) (LEUKOCYTE ANTIGEN F).// 4.80E-131// 158aa// 93%//
 P33617
 MESAN2001979
 35 MESAN2006563
 MESAN2012054

MESAN2014295
 MESAN2015515
 MESAN2018576
 MESTC1000042
 5 MESTC2000153
 NB9N41000340
 NCRRP1000129
 NESOP2000744
 NESOP2001433// ALC1_HUMAN Ig alpha-1 chain C region// 0// 353aa// 100%//
 10 P01876
 NESOP2001656
 NESOP2001694// H. sapiens graf gene.// 7.4E-53// 162aa// 66%// Y10388
 NESOP2001752
 NESOP2002738
 15 NHNPC2000606
 NHNPC2000877
 NHNPC2001223
 NHNPC2001816
 NHNPC2002565
 20 NHNPC2002749
 NOVAR2000136// Calsequestrin, skeletal muscle isoform precursor (Aspartactin)
 (Laminin-binding protein).// 1.00E-142// 235aa// 66%// P07221
 NOVAR2000710
 NOVAR2000962
 25 NOVAR2001108// Human (hybridoma H210) anti-hepatitis A IgG variable region,
 constant region, complementarity-determining regions mRNA, complete cds.//
 3.0E-230// 482aa// 88%// M87789
 NOVAR2001783
 NT2NE2003252// Human putative serine/threonine protein kinase PRK (prk) mRNA,
 30 complete cds.// 3.00E-44// 234aa// 38%// U56998
 NT2NE2005890
 NT2NE2006531// ZINC FINGER PROTEIN 184 (FRAGMENT).// 4.10E-113// 437aa//
 47%// Q99676
 NT2NE2006909// Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2)
 35 (Peptidase M 2) (Initiation factor 2 associated 67 kDa glycoprotein) (P67).//
 1.00E-147// 258aa// 80%// P50579

NT2NE2008060
 NT2RI2003993
 NT2RI2004618// Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2)
 (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase)
 5 (BACH).// 1.00E-126// 222aa// 88%// 000154
 NT2RI2005166// VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.// 7.70E-14//
 300aa// 26%// Q00808
 NT2RI2006686// E1A-ASSOCIATED PROTEIN P300.// 1.30E-18// 421aa// 26%// Q09472
 NT2RI2008724
 10 NT2RI2009855
 NT2RI2011422// Homo sapiens partial mRNA for transport-secretion protein 2.1
 (TTS-2.1 gene).// 6.4E-70// 428aa// 40%// AJ278475
 NT2RI2011683
 NT2RI2012659
 15 NT2RI2012990// 76.5 KDA PROTEIN C21ORF13.// 1.8E-73// 149aa// 100%// 095447
 NT2RI2013357
 NT2RI2014247
 NT2RI2014551
 NT2RI2014733
 20 NT2RI2016128
 NT2RI2018311
 NT2RI2018883
 NT2RI2019751
 NT2RI2023303
 25 NT2RI2025909// carnitine/acylcarnitine translocase// 3.0E-32// 260aa// 37%//
 NP_000378
 NT2RI2025957// LU1 protein [Homo sapiens]// 0// 630aa// 99%// AAF74512
 NT2RI2027081
 NT2RI2027396
 30 NT2RI3000622
 NT2RI3001263
 NT2RI3001515// ALEX1 protein [Homo sapiens]// 2.0E-25// 220aa// 29%//
 NP_057692
 NT2RI3002303
 35 NT2RI3002842
 NT2RI3002892

NT2RI3003031
 NT2RI3003095
 NT2RI3003162
 NT2RI3003382
 5 NT2RI3003409
 NT2RI3004381
 NT2RI3004510
 NT2RI3005202
 NT2RI3005403
 10 NT2RI3005724
 NT2RI3006132
 NT2RI3006171// CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN
 100) (CD66E ANTIGEN).// 1.3E-54// 294aa// 39%// P06731
 NT2RI3006284// Homo sapiens chorea-acanthocytosis (CHAC) mRNA, complete
 15 cds.// 1.2E-144// 538aa// 51%// AF337532
 NT2RI3006340// Myomesin 1 (Skelemin).// 0// 1390aa// 81%// Q62234
 NT2RI3006376
 NT2RI3006673// LAR protein precursor (Leukocyte antigen related) (EC
 3.1.3.48).// 0// 1151aa// 90%// P10586
 20 NT2RI3006796
 NT2RI3007065
 NT2RI3007158
 NT2RI3007291
 NT2RI3007543
 25 NT2RI3007757// breast cancer nuclear receptor-binding auxiliary protein //
 1.00E-172// 295aa// 94%// AAD21311
 NT2RI3007978// CTP synthase II: CTP synthetase type 2 [Homo sapiens]// 0//
 536aa// 91%// NM_019857
 NT2RI3008055
 30 NT2RI3008162
 NT2RI3008652// Homo sapiens mRNA for CDEP, complete cds.// 6.10E-113//
 443aa// 52%// AB008430
 NT2RI3008697// erythroblast macrophage protein [Mus musculus]// 2.00E-14//
 70aa// 25%// NM_021500
 35 NT2RI3008974// probable transposase - human transposon MER37// 1.20E-52//
 165aa// 69%// S72481

- NT2RI3009158// Iroquois-class homeodomain protein IRX-3.// 4.00E-16// 52aa// 36%// P81067
- NT2RP7000359// PROTEIN-TYROSINE PHOSPHATASE D1 (EC 3.1.3.48).// 6.80E-25// 319aa// 28%// Q16825
- 5 NT2RP7000466// Cegp1 protein// 0// 482aa// 89%// NP_064436
- NT2RP7004027// BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).// 9.50E-33// 301aa// 30%// P98063
- NT2RP7004123
- NT2RP7005118// RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195) (KIAA0051).// 0// 1034aa// 58%// P46940
- 10 NT2RP7005529// PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE).// 5.40E-56// 364aa// 37%// Q12774
- NT2RP7005846
- 15 NT2RP7009030
- NT2RP7009147// CHE-2 protein [Caenorhabditis elegans]// 1.00E-177// 740aa// 41%// CAB38019
- NT2RP7009867
- NT2RP7010128
- 20 NT2RP7010599// Homo sapiens endothelial lipase mRNA, complete cds.// 5.60E-174// 321aa// 98%// AF118767
- NT2RP7011570
- NT2RP7013795// VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.// 4.90E-11// 129aa// 34%// Q00808
- 25 NT2RP7014005// CTP synthase II; CTP synthetase type 2 [Homo sapiens]// 0// 536aa// 91%// NM_019857
- NT2RP7015512
- NT2RP7017365
- NT2RP7017474
- 30 NT2RP7017546
- NT2RP8000137
- NT2RP8000296// similar to Kelch proteins// 0// 600aa// 99%// AAF03529
- NT2RP8000483// Rattus norvegicus mRNA for Nadrin E2, complete cds.// 2.00E-208// 548aa// 75%// AB060557

- NTONG2000413// MATRIX METALLOPROTEINASE-16 PRECURSOR (EC 3.4.24.-) (MMP-16) (MEMBRANE-TYPE MATRIX METALLOPROTEINASE 3) (MT-MMP 3) (MTMMP3) (MMP-X2).// 5.60E-62// 290aa// 37%// P51512
- NTONG2003852
- 5 NTONG2005277// ANKYRIN 1 (ERYTHROCYTE ANKYRIN).// 8.20E-31// 363aa// 31%// Q02357
- NTONG2005969
- NTONG2006354
- NTONG2007249
- 10 NTONG2007517// RING CANAL PROTEIN (KELCH PROTEIN).// 9.10E-32// 295aa// 28%// Q04652
- NTONG2008088
- NTONG2008672// final exon in repeat region: similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein //
- 15 1.9E-15// 559aa// 25%// AAC48204
- OCBBF1000254
- OCBBF2001794
- OCBBF2002124// p40 [Homo sapiens]// 3.00E-63// 103aa// 88%// AAC51270
- OCBBF2003819
- 20 OCBBF2004826// T-cell lymphoma invasion and metastasis 2 [Homo sapiens]// 0// 580aa// 99%// NP_036586
- OCBBF2004883
- OCBBF2005428
- OCBBF2006005// Bos taurus phosphatidic acid-preferring phospholipase A1 mRNA, complete cds.// 0// 885aa// 90%// AF045022
- 25 OCBBF2006058// Homo sapiens acyl-Coenzyme A dehydrogenase-8 precursor, mRNA, complete cds.// 5.40E-57// 109aa// 100%// AF126245
- OCBBF2006151// Mus musculus protein tyrosine phosphatase-like protein PTPLB (Ptp1b) mRNA, complete cds.// 3.40E-126// 258aa// 93%// AF169286
- 30 OCBBF2006567
- OCBBF2006764// seizure related gene 6 [Mus musculus]// 0// 780aa// 89%// NP_067261
- OCBBF2007028// Homo sapiens mRNA for NESCA, complete cds.// 1.50E-169// 176aa// 98%// AB026894
- 35 OCBBF2007068// ankyrin 1 [Bos taurus].// 1.00E-68// 800aa// 32%// AAF61702
- OCBBF2007114

OCBBF2007428
 OCBBF2007478
 OCBBF2007610// PSD-95/SAP90-associated protein-4 [Rattus norvegicus].//
 1.00E-137// 226aa// 90%// AAB48590
 5 OCBBF2008770
 OCBBF2009788
 OCBBF2009926
 OCBBF2010140
 OCBBF2010416
 10 OCBBF2017516
 OCBBF2019327
 OCBBF2019823// lactate dehydrogenase A -like [Homo sapiens]// 1.00E-164//
 273aa// 82%// NM_033195
 OCBBF2020343
 15 OCBBF2020453
 OCBBF2020639
 OCBBF2020741
 OCBBF2020801// Ataxin 7 (Spinocerebellar ataxia type 7 protein).// 5.00E-67//
 116aa// 100%// 015265
 20 OCBBF2020838// FORKHEAD BOX PROTEIN D4 (FORKHEAD-RELATED PROTEIN FKHL9)
 (FORKHEAD- RELATED TRANSCRIPTION FACTOR 5) (FREAC-5) (TRANSCRIPTION FACTOR
 FKH- 2).// 1.70E-114// 371aa// 63%// Q60688
 OCBBF2021020// Homo sapiens mRNA for vascular Rab-GAP/TBC-containing protein,
 complete cds.// 1.8E-24// 107aa// 47%// AB024057
 25 OCBBF2021286
 OCBBF2021323// Mus musculus GTRGE022 (Gtrgeo22) mRNA, complete cds.// 7.80E-
 49// 115aa// 88%// AF303106
 OCBBF2021788// Homo sapiens mRNA for B-cell CLL/lymphoma 9 (BCL9 gene).//
 1.30E-92// 600aa// 42%// Y13620
 30 OCBBF2022351// TIPD PROTEIN.// 1.1E-54// 263aa// 40%// 015736
 OCBBF2022574
 OCBBF2023162
 OCBBF2023643
 OCBBF2024719
 35 OCBBF2024781
 OCBBF2024850

OCBBF2025028
OCBBF2025458
OCBBF2025527// GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC (EC
1.1.1.8) (GPD-C) (GPDH-C).// 8.60E-49// 116aa// 78%// P13707
5 OCBBF2025730
OCBBF2026645
OCBBF2027423
OCBBF2027478
OCBBF2028173// JM11 protein [Homo sapiens]// 1.00E-131// 304aa// 97%//
10 AAF05832
OCBBF2028935
OCBBF2029901
OCBBF2030354// Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA,
complete cds.// 9.50E-195// 372aa// 96%// AF200357
15 OCBBF2030517
OCBBF2030574
OCBBF2030708
OCBBF2031167// Homo sapiens mRNA for MDC2 alpha, MDC2 beta, complete cds.//
0// 813aa// 99%// AB009671
20 OCBBF2031366
OCBBF2032590// H.sapiens mRNA for melanoma-associated chondroitin sulfate
proteoglycan (MCSP).// 1.80E-11// 151aa// 39%// X96753
OCBBF2032599
OCBBF2032611
25 OCBBF2032671
OCBBF2033869// PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR (PCPE)
(TYPE I PROCOLLAGEN COOH-TERMINAL PROTEINASE ENHANCER) (TYPE 1 PROCOLLAGEN C-
PROTEINASE ENHANCER PROTEIN).// 6.6E-21// 151aa// 38%// Q15113
OCBBF2035110
30 OCBBF2035214
OCBBF2035564
OCBBF2035885
OCBBF2035916
OCBBF2036476
35 OCBBF2036743// ZINC FINGER PROTEIN 133.// 9.00E-157// 639aa// 48%// P52736

- OCBBF2037068// BCL2/adenovirus E1B 19-kDa protein-interacting protein 2.//
3.00E-74// 122aa// 66%// 054940
OCBBF2037340// Sacsin.// 0// 356aa// 100%// Q9NZJ4
OCBBF2037398
- 5 OCBBF2037547// T-cell lymphoma invasion and metastasis 2 [Homo sapiens]// 0//
1024aa// 92%// NM_012454
OCBBF2037598// axonal-associated cell adhesion molecule [Mus musculus]// 0//
366aa// 89%// NP_031544
OCBBF2037638
- 10 OCBBF2038317// VPS10 domain receptor protein SORCS [Mus musculus]// 0//
986aa// 91%// NM_021377
OCBBF3000296
OCBBF3000483
OCBBF3002553
- 15 OCBBF3002600
OCBBF3003320// Potential phospholipid-transporting ATPase 1S (EC 3.6.3.13)
(Fragment).// 1.00E-110// 179aa// 62%// P98196
OCBBF3003592// Dynein beta chain, flagellar outer arm.// 2.00E-54// 222aa//
21%// Q39565
- 20 OCBBF3004314// Fas apoptotic inhibitory molecule [Mus musculus]// 8.00E-67//
117aa// 90%// NM_011810
OCBBF3006802
OCBBF3007516
OCBBF3008230
- 25 OCBBF3009279
PEBLM2000170// Sprouty homolog 3 (Spry-3).// 1.00E-31// 64aa// 100%// 043610
PEBLM2000338
PEBLM2001465// diphthamide biosynthesis; Dph5p [Saccharomyces cerevisiae]//
9.00E-65// 160aa// 57%// NP_013273
- 30 PEBLM2001488
PEBLM2002594// ATP-binding cassette, sub-family A member 8 [Homo sapiens]//
4.50E-156// 469aa// 64%// XP_016390
PEBLM2002749
PEBLM2002887// ZINC FINGER PROTEIN 195.// 1.50E-08// 62aa// 58%// 014628
- 35 PEBLM2004497
PEBLM2004666

PEBLM2005183// 5'-3' exonuclease // 0// 804aa// 92%// CAA62819
 PEBLM2005697
 PEBLM2006113
 PEBLM2007112
 5 PEBLM2007140
 PEBLM2007834
 PERIC1000147
 PERIC2000889// Rattus norvegicus dynamin-like protein variant 4 mRNA,
 alternatively spliced, partial cds.// 3.1E-22// 51aa// 98%// AF107048
 10 PERIC2000914
 PERIC2001227
 PERIC2001228
 PERIC2002766
 PERIC2003090
 15 PERIC2003452
 PERIC2003699
 PERIC2003720// kinectin 1: CG-1 antigen [Homo sapiens].// 2.00E-92// 270aa//
 90%// NP_004977
 PERIC2003834
 20 PERIC2004028// Mus musculus erythroblast macrophage protein EMP mRNA,
 complete cds.// 3.80E-33// 65aa// 100%// AF263247
 PERIC2004259
 PERIC2004379
 PERIC2004429
 25 PERIC2004909
 PERIC2005347// alpha 1C adrenergic receptor isoform 2// 3.30E-22// 74aa//
 70%// BAA06901
 PERIC2005370
 PERIC2006035
 30 PERIC2007914// Ubiquitously transcribed TPR gene on Y chromosome [Homo
 sapiens]// 1.0E-22// 84aa// 67%// NP_009056
 PERIC2008385// sarcosine dehydrogenase; dimethylglycine dehydrogenase-like 1
 [Homo sapiens]// 4.00E-17// 47aa// 51%// NM_007101
 PERIC2009086// Homo sapiens melanoma-associated antigen MG50 mRNA, partial
 35 cds.// 5.00E-189// 508aa// 66%// AF200348
 PLACE5000001

- PLACE5000171// E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).// 1.50E-28// 242aa// 30%// P98110
PLACE5000260
- 5 PLACE5000282// elastin [Homo sapiens]// 8.00E-08// 420aa// 97%// NP_000492
PLACE6001185
PLACE6009006
PLACE6012574
PLACE6019385// MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 5 (EC 2.7.1.-)
- 10 (MAPK/ERK KINASE KINASE 5) (MEK KINASE 5) (MEKK 5) (APOPTOSIS SIGNAL-REGULATING KINASE 1) (ASK-1).// 2E-57// 92aa// 63%// Q99683
PLACE6019932// Ictalurus punctatus NCC receptor protein 1 (NCCRP-1) mRNA, complete cds.// 1.2E-34// 124aa// 50%// AF208795
PLACE6020031// ANKYRIN HOMOLOG PRECURSOR.// 2.70E-06// 156aa// 35%// Q06527
- 15 PLACE7000514// Mus musculus mRNA for ER protein 58 (EP58 gene).// 3.80E-111// 366aa// 55%// AJ404004
PLACE7001022
PLACE7001936
PLACE7002641// Ring assembly protein 3.// 2.00E-13// 79aa// 26%// 074994
- 20 PLACE7006051// cytoplasmic dynein heavy chain 2 [Rattus norvegicus]// 0// 987aa// 90%// NM_023024
PLACE7008431// Phosphatidylinositol-4-phosphate 5-kinase type II alpha (EC 2.7.1.68) (PIP5KII-alpha) (1-phosphatidylinositol-4-phosphate kinase) (PtdIns(4)P-5-kinase B isoform) (Diphosphoinositide kinase).// 1.00E-109//
- 25 200aa// 56%// 070172
PLACE7008623
PROST1000184// VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP-R-2).// 7.0E-63// 125aa// 98%// P32241
- 30 PROST1000528
PROST1000559// predicted osteoblast protein [Homo sapiens]// 6.00E-33// 227aa// 38%// NP_055703
PROST2003428// Protein pM5 precursor.// 9.00E-47// 91aa// 89%// Q15155
PROST2008993// Mus musculus Pax transcription activation domain interacting protein PTIP mRNA, complete cds.// 1.10E-211// 542aa// 77%// AF104261
- 35 PROST2015243

- PROST2016462// N-chimaerin (NC) (N-chimerin) (Alpha chimerin) (A-chimaerin).// 6.00E-26// 65aa// 34%// P30337
- PROST2017367// PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE 4 (EC 2.3.2.13) (PROSTATE TRANSGLUTAMINASE) (PROSTATE TRANSGLUTAMINASE) (TGP).// 1.30E-52//
- 5 102aa// 99%// P49221
- PROST2017413
- PROST2017700
- PROST2018030
- PROST2018090// SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR.// 9.50E-244//
- 10 414aa// 99%// P78539
- PROST2018511// Growth factor receptor-bound protein 7 (GRB7 adapter protein) (Epidermal growth factor receptor GRB-7) (B47).// 0// 495aa// 99%// Q14451
- PROST2018902
- PROST2018922
- 15 PROST2019296
- PROST2019781
- PUAEN2002489// Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds.// 1.0E-48// 189aa// 53%// AF027826
- PUAEN2002616
- 20 PUAEN2003079// nasopharyngeal carcinoma susceptibility protein [Homo sapiens]// 3.00E-36// 75aa// 96%// NP_037407
- PUAEN2005588
- PUAEN2005930
- PUAEN2006328// vascular Rab-GAP/TBC-containing [Homo sapiens]// 8.0E-99//
- 25 360aa// 53%// NP_008994
- PUAEN2006701
- PUAEN2007044// TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).// 7.90E-15// 129aa// 34%// P45142
- 30 PUAEN2007785
- PUAEN2009174
- PUAEN2009655// Bos taurus phosphatidic acid-preferring phospholipase A1 mRNA, complete cds.// 0// 565aa// 96%// AF045022
- PUAEN2009795// Endothelial cell multimerin precursor.// 1.00E-161// 296aa//
- 35 78%// Q13201

- PUAEN2009852// serine/threonine protein kinase Kp78 splice variant CTAK75a // 3.00E-33// 86aa// 36%// AAD48007
RECTM2000433// ZG-16p [Rattus norvegicus] // 1.60E-64// 148aa// 85%// CAA83059
- 5 RECTM2001347// sphingosine kinase type 2 isoform [Homo sapiens]// 4.00E-46// 87aa// 80%// NM_020126
SKMUS2000757
SKMUS2003074
SKMUS2004047
- 10 SKMUS2006394// Mus musculus ankyrin repeat-containing protein Asb-4 mRNA, partial cds.// 6.40E-54// 405aa// 34%// AF155355
SKNMC1000124// putative nuclear protein [Homo sapiens].// 3.00E-12// 398aa// 37%// NP_057689
SKNMC2002402
- 15 SKNMC2004457
SKNMC2004643
SKNMC2005772
SKNMC2006998// PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (I-1).// 9.9E-32// 113aa// 64%// Q13522
- 20 SKNMC2007504// DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) (RPB1).// 1.00E-16// 76aa// 26%// P08775
SKNMC2007961
SKNMC2009450
SKNSH2000482
- 25 SKNSH2009991
SKNSH2010015
SMINT1000192// PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0134.// 4.00E-12// 37aa// 100%// Q14147
SMINT2001818
- 30 SMINT2002743
SMINT2006641
SMINT2007391
SMINT2009902
SMINT2010076// Ig alpha-1 chain C region.// 0// 319aa// 91%// P01876
- 35 SMINT2010897
SMINT2011311

- SMINT2011888// protein Tro alpha1 H, myeloma// 8.9E-215// 481aa// 82%//
0501254A
- SMINT2015787// immunoglobulin lambda light chain [Homo sapiens]// 1.40E-60//
164aa// 77%// CAA40954
- 5 SPLEN2001599// Homo sapiens sialic acid binding immunoglobulin-like lectin 8
long splice variant (Siglec8) gene, complete cds.// 4.00E-71// 294aa// 38%//
AF287892
- SPLEN2002147// Halocynthia roretzi mRNA for HrPET-3, complete cds.// 1.20E-
09// 78aa// 41%// AB029335
- 10 SPLEN2002467// Homo sapiens leucine-rich repeats containing F-box protein
FBL3 mRNA, complete cds.// 1.60E-187// 422aa// 77%// AF186273
- SPLEN2002707
- SPLEN2006122// Homo sapiens RNA-binding region (RNP1, RRM) containing 2
(RNPC2)// 2.00E-81// 147aa// 84%// NM_004902
- 15 SPLEN2009548
- SPLEN2010912// putative nucleolar RNA helicase [Homo sapiens]// 0// 339aa//
90%// NM_019082
- SPLEN2011422// CALDESMON (CDM).// 5.3E-12// 165aa// 37%// Q05682
- SPLEN2012624// BRCA1-associated RING domain protein 1 (BARD-1).// 6.00E-14//
20 48aa// 39%// Q9QZH2
- SPLEN2012889// putative Na⁺-dependent inorganic phosphate cotransporter//
9.00E-19// 70aa// 32%// AAC35230
- SPLEN2014946
- SPLEN2015158
- 25 SPLEN2015267// Homo sapiensIGHG3 gene for immunoglobulin heavy chain gamma 3
constant region, 4-exon hinge, isolate Lib-A2.// 1.0E-213// 377aa// 100%//
AJ390247
- SPLEN2015679// Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA,
complete cds.// 4.90E-30// 266aa// 31%// U21157
- 30 SPLEN2016554
- SPLEN2016863
- SPLEN2017104
- SPLEN2021701// HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA CHAIN
PRECURSOR.// 4.40E-128// 173aa// 86%// P01892
- 35 SPLEN2023733
- SPLEN2023791

SPLN2024127
SPLN2025491
SPLN2027268
SPLN2028844
5 SPLN2028914
SPLN2029051
SPLN2029176
SPLN2029522
SPLN2029683
10 SPLN2029727
SPLN2029912
SPLN2030335// Mus musculus fatty acid transport protein 3 mRNA, partial
cds// 9.7E-251// 275aa// 81%// AF072758
SPLN2030479
15 SPLN2031125
SPLN2031424
SPLN2031547// Triose phosphate/phosphate translocator, non-green plastid
precursor (CTPT).// 4.00E-20// 76aa// 25%// P52178
SPLN2031724
20 SPLN2031780
SPLN2032154// NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1)
(REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC
INDUCTION PROTEIN CAP43).// 1.0E-22// 80aa// 57%// Q92597
SPLN2032321
25 SPLN2032813
SPLN2033098// tumor necrosis factor receptor superfamily, member 14// 1.7E-
99// 183aa// 100%// NP_003811
SPLN2033153
SPLN2033539
30 SPLN2033921
SPLN2034021
SPLN2034081
SPLN2034678
SPLN2034781
35 SPLN2036103

SPLEN2036326// CLAUDIN-5 (TRANSMEMBRANE PROTEIN DELETED IN VCFS) (TMDVCF).//
 2.6E-118// 218aa// 100%// 000501
 SPLEN2036712
 SPLEN2036821// MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN
 5 (CARNITINE/ACYLCARNITINE TRANSLOCASE) (CAC).// 6.5E-10// 104aa// 33%// 043772
 SPLEN2036932// Homo sapiens calcium and DAG-regulated guanine nucleotide
 exchange factor I mRNA, complete cds.// 3.9E-63// 124aa// 100%// AF081194
 SPLEN2037194// NORQ PROTEIN.// 5.5E-11// 127aa// 38%// Q51664
 SPLEN2037580
 10 SPLEN2037630
 SPLEN2037722// lymphocyte antigen 108 [Mus musculus]// 3.00E-63// 137aa//
 42%// NM_030710
 SPLEN2038055
 SPLEN2038180
 15 SPLEN2038345
 SPLEN2038407// basement membrane-induced gene // 2.1E-33// 283aa// 34%//
 XP_001646
 SPLEN2039697
 SPLEN2039936
 20 SPLEN2040222
 SPLEN2041304
 SPLEN2041310
 SPLEN2041645
 SPLEN2041720
 25 SPLEN2041977
 SPLEN2042303
 SPLEN2042598
 STOMA1000189
 STOMA2003444
 30 STOMA2004294// Ig lambda chain V-IV region Bau.// 1.00E-41// 79aa// 73%//
 P01715
 STOMA2004925
 STOMA2008546// CDM PROTEIN (6C6-AG TUMOR-ASSOCIATED ANTIGEN) (DXS1357E).//
 5.00E-124// 246aa// 100%// P51572
 35 SYN0V1000374

SYNOV2005216// Homo sapiens laryngeal carcinoma related protein 1 mRNA,
 complete cds.// 2.5E-36// 70aa// 98%// AF268387
 SYNOV2005448
 SYNOV2005817// CYTOKINE RECEPTOR CLASS-III CRF2-4 PRECURSOR.// 7.6E-176//
 5 314aa// 98%// Q08334
 SYNOV2006430
 SYNOV2007965// Homo sapiens mRNA for H-I(3)mbt-like protein, alternative
 variant a.// 3.1E-118// 429aa// 54%// AJ305226
 SYNOV2012326// PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48).//
 10 6.7E-24// 112aa// 58%// P56180
 SYNOV2014400// FIBULIN-1, ISOFORM C PRECURSOR.// 4.0E-31// 198aa// 37%//
 P23144
 SYNOV2016124
 SYNOV2017055
 15 SYNOV2018921
 SYNOV2021320// SH3 DOMAIN-BINDING PROTEIN 3BP-2.// 2.3E-238// 429aa// 98%//
 P78314
 SYNOV3000231// Ig gamma-1 chain C region.// 0// 315aa// 95%// P01857
 SYNOV3000302// Ig gamma-1 chain C region.// 1.00E-173// 294aa// 89%// P01857
 20 SYNOV4000472
 SYNOV4000706// B cell phosphoinositide 3-kinase adaptor [Mus musculus]// 0//
 633aa// 79%// NM_031376
 SYNOV4001326
 SYNOV4001395
 25 SYNOV4002346
 SYNOV4002392
 SYNOV4002883// S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50)
 (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain;
 S-adenosylmethionine decarboxylase beta chain].// 4.00E-72// 129aa// 99%//
 30 P17707
 SYNOV4003322
 SYNOV4004184
 SYNOV4004741// BENE protein (Fragment).// 2.00E-77// 140aa// 94%// Q13021
 SYNOV4004823
 35 SYNOV4004914
 SYNOV4006256

SYNOV4007012
 SYNOV4007215
 SYNOV4007360// SSXT protein (SYT protein).// 5.00E-24// 70aa// 36%// Q62280
 SYNOV4007430
 5 SYNOV4007521// fibroblast growth factor receptor-like 1 precursor [Homo
 sapiens]// 7.00E-11// 53aa// 29%// NM_021923
 SYNOV4007553// toll-like receptor2 [Homo sapiens]// 0// 740aa// 94%//
 NM_003264
 SYNOV4007671// Syntaxin 3.// 1.00E-144// 262aa// 99%// Q13277
 10 SYNOV4008336
 SYNOV4008440// Protein BAP28.// 0// 1119aa// 85%// Q9H583
 T1ESE2000116
 TBAES2001171
 TBAES2001220
 15 TBAES2001229// 60S ribosomal protein L23a.// 8.00E-48// 92aa// 82%// P29316
 TBAES2001258// SERINE PROTEASE HEPsin (EC 3.4.21.-) (TRANSMEMBRANE PROTEASE,
 SERINE 1).// 6.40E-19// 55aa// 87%// P05981
 TBAES2001492
 TBAES2001751
 20 TBAES2002197
 TBAES2003550
 TBAES2004055// NY-REN-50 antigen// 1.00E-155// 290aa// 99%// AAD42878.
 TBAES2005157
 TBAES2005543
 25 TBAES2006568
 TBAES2007964
 TCERX2000613
 TCOLN2002278
 TESOP1000127
 30 TESOP2000801// PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112)
 (P61-YES) (C-YES).// 3.9E-46// 159aa// 57%// Q04736
 TESOP2001122// Caenorhabditis elegans LIN-9S (lin-9) mRNA, complete cds.//
 5.60E-25// 222aa// 28%// AF269694
 TESOP2001166// Mus musculus SOCS-5 mRNA, complete cds.// 1.2E-114// 439aa//
 35 53%// AF033187
 TESOP2001345

- TESOP2001605// Homo sapiens laryngeal carcinoma related protein 1 mRNA,
complete cds.// 2.5E-36// 70aa// 98%// AF268387
- TESOP2001818
- TESOP2001849
- 5 TESOP2001865
- TESOP2001953// ooplasm [Mus musculus]// 7.00E-08// 58aa// 26%// NM_011860
- TESOP2002273
- TESOP2002451
- TESOP2002489
- 10 TESOP2002539
- TESOP2002950
- TESOP2003273
- TESOP2003753
- TESOP2004114// PROCOLLAGEN-LYSINE, 2-OXOGLUTARATE 5-DIOXYGENASE 2 PRECURSOR
15 (EC 1.14.11.4) (LYSYL HYDROXYLASE 2) (LH2).// 1.70E-202// 237aa// 99%//
000469
- TESOP2005285// Homo sapiens partial mRNA for chr2 synaptotagmin (CHR2SYT
gene).// 1.1E-21// 54aa// 96%// AJ303365
- TESOP2005485// Ig delta chain C region.// 2.00E-77// 136aa// 100%// P01880
- 20 TESOP2005579
- TESOP2006041
- TESOP2006060
- TESOP2006068
- TESOP2006670
- 25 TESOP2006746
- TESOP2007052
- TESOP2007262
- TESOP2007636
- TESOP2007688
- 30 TESOP2009121// Homo sapiens centromere protein E (312kD) (CENPE), mRNA//
2.00E-10// 155aa// 20%// NM_001813
- TESOP2009555
- TEST11000257// GLUCOSE TRANSPORTER TYPE 3, BRAIN.// 7.4E-249// 493aa// 95%//
P11169
- 35 TEST11000319// Putative eukaryotic translation initiation factor 3 subunit
(eIF-3) (Fragment).// 0// 683aa// 97%// 075153

TESTI1000330
 TESTI1000348
 TESTI1000390
 TESTI1000491
 5 TESTI1000545// Ring assembly protein 3.// 2.00E-14// 92aa// 26%// 074994
 TESTI2000443
 TESTI2000644// SMALL INDUCIBLE CYTOKINE A14 PRECURSOR (CHEMOKINE CC-1/CC-3)
 (HCC-1/HCC-3) (NCC-2).// 2.80E-36// 69aa// 98%// Q16627
 TESTI2002036// DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM
 10 CHANNEL ALPHA-1 SUBUNIT.// 1.70E-18// 398aa// 24%// P22316
 TESTI2002618// ADAM 2 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE DOMAIN
 2) (FERTILIN BETA SUBUNIT) (PH-30) (PH30).// 1.10E-57// 253aa// 47%// Q99965
 TESTI2002928
 TESTI2003347// Homo sapiens connexin 59 (CX59) gene, complete cds.// 1.80E-
 15 243// 440aa// 100%// AF179597
 TESTI2003573// Mus musculus cell cycle checkpoint control protein Mrad9 gene,
 complete cds.// 2.4E-38// 325aa// 30%// AF045662
 TESTI2004215// Maackia amurensis early nodulin (ENOD2) mRNA, partial cds.//
 1.3E-34// 390aa// 31%// AF039708
 20 TESTI2004700
 TESTI2005376
 TESTI2005610// H. sapiens encoding CLA-1 mRNA.// 5.9E-234// 425aa// 99%//
 Z22555
 TESTI2005739// Drosophila melanogaster Rho-kinase (Rhk) mRNA, complete cds.//
 25 1.7E-09// 383aa// 24%// AF151375
 TESTI2005986
 TESTI2006041
 TESTI2006643
 TESTI2006648// ATP-binding cassette, sub-family C, member 5a// 9E-109//
 30 452aa// 39%// NP_038818
 TESTI2009474
 TESTI2009477// TRICHOHYALIN.// 1.9E-18// 124aa// 39%// P37709
 TESTI2009511
 TESTI2009812
 35 TESTI2010400
 TESTI2013381

- TESTI2013382
 TESTI2014716// G-RICH SEQUENCE FACTOR-1 (GRSF-1).// 2.6E-228// 391aa// 99%//
 Q12849
 TESTI2014843
- 5 TESTI2016046// Homo sapiens HOTTTL protein mRNA, complete cds.// 2.8E-20//
 242aa// 26%// AF078842
 TESTI2017727
 TESTI2018838
 TESTI2019042
- 10 TESTI2019648
 TESTI2023254
 TESTI2023599
 TESTI2024567// METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.// 1.10E-130//
 243aa// 99%// 000222
- 15 TESTI2026505// PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC
 GEF) (FACIOGENITAL DYSPLASIA PROTEIN).// 1.40E-50// 378aa// 29%// P98174
 TESTI2027019// Homo sapiens leucine-rich repeat-containing G protein-coupled
 receptor 6 (LGR6) mRNA, partial cds.// 4.80E-125// 137aa// 100%// AF190501
 TESTI2031529
- 20 TESTI2034520// Rattus norvegicus SMC (segregation of mitotic chromosomes 1)-
 like 1 (yeast) (Smc1l1), mRNA// 1.00E-145// 250aa// 53%// NM_031683
 TESTI2034749
 TESTI2034767// Homo sapiens collagen type IX alpha 1 chain (COL9A1) gene,
 long and short alternatively spliced forms, exon 38 and complete cds.//
 1.40E-191// 484aa// 73%// AF036130
- 25 TESTI2034953// Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.//
 2.00E-27// 91aa// 64%// AF204231
 TESTI2034997
 TESTI2035107
- 30 TESTI2035997
 TESTI2036513
 TESTI2036684
 TESTI2037643
 TESTI2040018// Homo sapiens ZNF258 (ZNF258) mRNA, complete cds.// 7.80E-97//
 461aa// 49%// AF055470
- 35 TESTI2042450

TESTI2044796// ring finger protein 3 [Homo sapiens]// 9.00E-41// 92aa// 38%//
NM_006315
TESTI2044833
TESTI2045920
5 TESTI2045983
TESTI2046347
TESTI2047071
TESTI2048465
TESTI2048603
10 TESTI2048898
TESTI2049206
TESTI2049246
TESTI2049277
TESTI2049422
15 TESTI2049452
TESTI2049469
TESTI2049576
TESTI2049857// golgi stacking protein homolog GRASP55 [Rattus norvegicus]//
5.00E-163// 410aa// 89%// AAD55350
20 TESTI2050137// SHC transforming protein.// 1.00E-113// 232aa// 54%// P98083
TESTI2050681
TESTI2050987// RET finger protein-like 1.// 4.00E-35// 94aa// 34%// 075677
TESTI2051279
TESTI2051488
25 TESTI2051543
TESTI2051767
TESTI2051806
TESTI2051867// 60S ribosomal protein L4 (L1).// 1.00E-126// 222aa// 86%//
P36578
30 TESTI2052211
TESTI2052693// brk kinase substrate [Homo sapiens].// 0// 341aa// 87%//
CAB65105
TESTI2052698
TESTI2052822
35 TESTI2053242

- TESTI2053399// Homo sapiens pescadillo homolog 1, containing BRCT domain (zebrafish) (PES1), mRNA// 9.00E-33// 63aa// 100%// NM_014303
- TESTI2053526
- 5 TESTI2053621// Guanylyl cyclase activating protein 1 (GCAP 1) (Guanylate cyclase activator 1A).// 7.00E-96// 170aa// 92%// P43080
- TESTI4000014// 130 kDa leucine-rich protein (LRP 130) (GP130).// 0// 1210aa// 96%// P42704
- TESTI4000068
- 10 TESTI4000079// nuclear dual-specificity phosphatase [Homo sapiens]// 6.00E-07// 80aa// 36%// AAC39675
- TESTI4000209// Homo sapiens F-BOX domain protein mRNA, complete cds.// 5.5E-103// 194aa// 99%// AF248640
- TESTI4000215
- TESTI4000250
- 15 TESTI4000288// Dynamin-1 (EC 3.6.1.50) (D100) (Dynamin, brain) (B-dynamin).// 2.00E-13// 38aa// 77%// P21575
- TESTI4000349// thyroid hormone receptor interactor 12// 1.00E-39// 180aa// 40%// NP_004229
- TESTI4000462
- 20 TESTI4000530
- TESTI4000724// solute carrier family 16 (monocarboxylic acid transporters)// 5.00E-47// 490aa// 28%// NP_004687
- TESTI4000970
- 25 TESTI4001100// protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [Homo sapiens]// 3.00E-21// 50aa// 40%// NM_003626
- TESTI4001106// ubiquitin-protein ligase e3 component n-recognin [Mus musculus]// 1.00E-124// 228aa// 45%// NM_009461
- TESTI4001148// Dynein beta chain, ciliary.// 1.00E-152// 282aa// 45%// P39057
- 30 TESTI4001176// Regulator of nonsense transcripts 1 (Nonsense mRNA reducing factor 1) (NORF1) (Up-frameshift suppressor 1 homolog).// 3.00E-46// 90aa// 92%// Q92900
- TESTI4001201
- TESTI4001206
- 35 TESTI4001527// UDP-glucuronosyltransferase 2C1 microsomal (EC 2.4.1.17) (UDPGT) (Fragment).// 9.00E-24// 64aa// 36%// P36514

TESTI4001561// 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma (EC 2.3.1.51) (1- AGP acyltransferase 3) (1-AGPAT 3) (Lysophosphatidic acid acyltransferase-gamma) (LPAAT-gamma) (1-acylglycerol-3-phosphate O-acyltransferase 3).// 0// 319aa// 93%// Q9NRZ7

5 TESTI4001665
TESTI4001923
TESTI4002290
TESTI4002491// Beta-soluble NSF attachment protein (SNAP-beta) (N-ethylmaleimide- sensitive factor attachment protein, beta) (Brain protein 147) (Fragment).// 1.00E-52// 99aa// 93%// P28663

10 TESTI4002552// Sodium/potassium-transporting ATPase alpha-4 chain (EC 3.6.3.9) (Sodium pump 4) (Na⁺/K⁺ ATPase 4) (Fragment).// 0// 505aa// 94%// Q13733
TESTI4002647

15 TESTI4002703
TESTI4002754
TESTI4002878
TESTI4004200
TESTI4005628

20 TESTI4005805
TESTI4005857
TESTI4005961
TESTI4006053
TESTI4006079// MUF1 protein; likely ortholog of mouse MUF1; elongin BC-interacting leucine-rich repeat protein [Homo sapiens]// 0// 365aa// 80%// NM_006369
TESTI4006112
TESTI4006137
TESTI4006148// putative NADH oxidoreductase complex I subunit// 2.00E-18// 40aa// 56%// AAD37863.

30 TESTI4006219
TESTI4006326
TESTI4006393// neural specific sr protein NSSR 2 [Mus musculus]// 7.00E-19// 70aa// 80%// BAA35093

35 TESTI4006412

- TESTI4006420// SH3-domain binding protein 5 (BTK-associated): SH3 binding protein [Homo sapiens]// 8.00E-25// 61aa// 41%// NM_004844
- TESTI4006546// colon cancer antigen NY-CO-45 [Homo sapiens].// 0// 723aa// 99%// AAC18034
- 5 TESTI4006802// mesothelin; megakaryocyte potentiating factor [Mus musculus]// 2.00E-06// 92aa// 23%// NM_018857
- TESTI4006819// Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (NON- neural enolase) (NNE) (Phosphopyruvate hydratase).// 1.00E-33// 72aa// 66%// P06733
- 10 TESTI4007064
- TESTI4007163// Sodium- and chloride-dependent creatine transporter 2 (CT2) (Fragment).// 2.00E-92// 153aa// 84%// P53796
- TESTI4007203
- TESTI4007239
- 15 TESTI4007373
- TESTI4007382
- TESTI4007404
- TESTI4007489
- TESTI4007775
- 20 TESTI4007778// Alpha-actinin 3 (Alpha actinin skeletal muscle isoform 3) (F-actin cross linking protein).// 0// 853aa// 94%// Q08043
- TESTI4007799
- TESTI4007810// DNA ligase III (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).// 1.00E-112// 197aa// 86%// P49916
- 25 TESTI4008007
- TESTI4008018// DAZ associated protein 2; KIAA0058 gene product [Homo sapiens]// 6.00E-41// 82aa// 75%// NM_014764
- TESTI4008050// Translocation protein SEC63 homolog.// 1.00E-175// 314aa// 82%// Q9UGP8
- 30 TESTI4008219
- TESTI4008401
- TESTI4008429// Probable cation-transporting ATPase 2 (EC 3.6.3.-) (CGI-152).// 1.00E-136// 249aa// 94%// Q9HD20
- TESTI4008573
- 35 TESTI4008797
- TESTI4008816

TESTI4008935
 TESTI4008993
 TESTI4009022
 TESTI4009034
 5 TESTI4009123
 TESTI4009160// Kinesin-like protein KIF2.// 6.00E-06// 39aa// 37%// P28740
 TESTI4009215
 TESTI4009283
 TESTI4009286// Homo sapiens HOTTTL protein mRNA, complete cds// 2.00E-78//
 10 180aa// 96%// AF078842
 TESTI4009374// Apobec-1 complementation factor; APOBEC-1 stimulating protein;
 apobec-1 complementation factor [Homo sapiens]// 1.00E-120// 203aa// 68%//
 NM_014576
 TESTI4009406
 15 TESTI4009457// p53-inducible p53DINP1 [Homo sapiens]// 3.00E-80// 140aa//
 88%// NM_033285
 TESTI4009563// testis specific ankyrin-like protein 1 [Homo sapiens]// 1.00E-
 140// 239aa// 94%// NM_017844
 TESTI4009608// putative T1/ST2 receptor binding protein [Homo sapiens]//
 20 1.00E-41// 125aa// 57%// NP_006849
 TESTI4009638
 TESTI4009881// Dynein heavy chain, cytosolic (DYHC) (Cytoplasmic dynein heavy
 chain).// 5.00E-30// 176aa// 21%// Q9JHU4
 TESTI4010211
 25 TESTI4010377
 TESTI4010713
 TESTI4010789
 TESTI4010817
 TESTI4010831// yeast Sec31p homolog; ABP125 [Homo sapiens]// 0// 780aa//
 30 81%// NM_016211
 TESTI4010851// Probable ubiquitin carboxyl-terminal hydrolase FAF-X (EC
 3.1.2.15) (Ubiquitin thiolesterase FAF-X) (Ubiquitin-specific processing
 protease FAF-X) (Deubiquitinating enzyme FAF-X) (Fat facets protein related,
 X-linked) (Ubiquitin-specific protease 9, X chromosome).// 2.00E-67// 213aa//
 35 25%// Q93008
 TESTI4010928

TESTI4011118
 TESTI4011161
 TESTI4011246
 TESTI4011484// Sec23-interacting protein p125 [Homo sapiens]// 0// 387aa//
 5 52%// NM_007190
 TESTI4011505
 TESTI4011745// WD-repeat protein 9 (Fragment).// 0// 674aa// 82%// Q9NSI6
 TESTI4011956// Ciliary dynein heavy chain (Axonemal dynein heavy chain)
 (Dynein heavy chain 9).// 1.00E-170// 340aa// 39%// Q9NYC9
 10 TESTI4012086
 TESTI4012329
 TESTI4012406// Apolipoprotein(A) (EC 3.4.21.-) (Apo(A)) (LP(A)) (Fragment).//
 2.00E-25// 50aa// 79%// P14417
 TESTI4012448// Stromelysin-3 precursor (EC 3.4.24.-) (Matrix
 15 metalloproteinase-11) (MMP-11) (ST3) (SL-3).// 0// 375aa// 99%// P24347
 TESTI4012505// Tumor suppressor p53-binding protein 2 (p53-binding protein 2)
 (53BP2) (Bcl2-binding protein) (Bbp).// 1.00E-81// 220aa// 34%// Q13625
 TESTI4012556
 TESTI4012679// Homo sapiens cryptochrome 1 (photolyase-like) (CRY1), mRNA//
 20 0// 330aa// 97%// NM_004075
 TESTI4012702
 TESTI4013369// ATP synthase lipid-binding protein, mitochondrial precursor
 (EC 3.6.1.34) (ATP synthase proteolipid P3) (ATPase protein 9) (ATPase
 subunit C).// 7.00E-60// 119aa// 83%// P48201
 25 TESTI4013667
 TESTI4013675
 TESTI4013685
 TESTI4013735
 TESTI4013817// novel AMP-binding enzyme similar to acetyl-coenzyme A
 30 synthetase (acetate-coA ligase)// 8.00E-38// 99aa// 100%// CAB75500
 TESTI4013830// Integral membrane glycoprotein gp210 precursor.// 0// 652aa//
 41%// P11654
 TESTI4013924// Intracellular protein transport protein US01.// 8.00E-20//
 125aa// 20%// P25386
 35 TESTI4014159

TESTI4014175// Chromodomain helicase-DNA-binding protein 3 (CHD-3) (Mi-2
 autoantigen 240 kDa protein) (Mi2-alpha).// 0// 410aa// 75%// Q12873
 TESTI4014306
 TESTI4014392
 5 TESTI4014445
 TESTI4014694
 TESTI4014818// AD-012 protein [Homo sapiens]// 1.00E-123// 217aa// 70%//
 NM_018449
 TESTI4014924// selective hybridizing clone [Mus musculus]// 0// 1153aa//
 10 92%// NM_011370
 TESTI4015263
 TESTI4015293
 TESTI4015471
 TESTI4015600
 15 TESTI4015646
 TESTI4015681
 TESTI4015688
 TESTI4016110// DnaJ homolog subfamily B member 8 (mDJ6).// 1.00E-91// 165aa//
 71%// Q9QYI7
 20 TESTI4016238
 TESTI4016551
 TESTI4016812
 TESTI4016822// Protein phosphatase inhibitor 2 (IPP-2).// 9.00E-72// 133aa//
 83%// P41236
 25 TESTI4016882
 TESTI4016925// Dynein beta chain, ciliary.// 0// 533aa// 34%// P39057
 TESTI4017001
 TESTI4017137
 TESTI4017254
 30 TESTI4017543// ubinuclein 1 [Homo sapiens]// 1.00E-124// 286aa// 38%//
 NM_016936
 TESTI4017575
 TESTI4017848
 TESTI4017901// alpha-1A-adrenergic receptor, isoform 2: adrenergic, alpha -
 35 1A-, receptor: adrenergic, alpha-1C-, receptor: alpha 1A-adrenoceptor [Homo
 sapiens]// 9.00E-21// 51aa// 72%// NM_033303

TESTI4017961

TESTI4018152// protein tyrosine phosphatase, non-receptor type 13 [Mus musculus]// 3.00E-18// 130aa// 33%// NP_035334.

TESTI4018208// MYOSIN IC HEAVY CHAIN.// 6.10E-07// 112aa// 40%// P10569

5 TESTI4018382

TESTI4018555

TESTI4018806

TESTI4018835// Potential phospholipid-transporting ATPase 1K (EC 3.6.3.13) (Fragment).// 0// 514aa// 88%// 060423

10 TESTI4018881// early endosome antigen 1, 162kD; early endosome-associated protein [Homo sapiens]// 2.00E-14// 101aa// 22%// NM_003566

TESTI4018886// M-protein, striated muscle.// 4.00E-81// 146aa// 46%// Q02173

TESTI4019140// Mi-2 histone deacetylase complex protein 66 [Xenopus laevis]// 2.00E-98// 410aa// 71%// AAD55392

15 TESTI4019299

TESTI4019417

TESTI4019566// Dosage compensation regulator (Male-less protein) (No action potential protein).// 8.00E-49// 165aa// 29%// P24785

TESTI4019843// Rattus norvegicus huntingtin-associated protein interacting protein (duo) (Hapip), mRNA.// 0// 698aa// 91%// NM_032062

TESTI4020092// Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain).// 3.00E-40// 74aa// 96%// P24043

TESTI4020102

TESTI4020806

25 TESTI4020920

TESTI4021294

TESTI4021456

TESTI4021478// Potential phospholipid-transporting ATPase 1S (EC 3.6.3.13) (Fragment).// 0// 433aa// 54%// P98196

30 TESTI4021491

TESTI4022716// RNA helicase [Homo sapiens]// 0// 817aa// 95%// NM_014314

TESTI4022873// Dynein gamma chain, flagellar outer arm.// 3.00E-09// 106aa// 19%// Q39575

TESTI4022936

35 TESTI4023546// Sialidase (EC 3.2.1.18) (Neuraminidase) (NA) (Major surface antigen).// 6.00E-32// 134aa// 23%// P23253

TESTI4023555
 TESTI4023722
 TESTI4023762// Trichohyalin. // 5.00E-12// 94aa// 22%// P37709
 TESTI4023942
 5 TESTI4024344
 TESTI4024420// multidomain presynaptic cytomatrix protein Piccolo [Rattus norvegicus]// 0// 789aa// 82%// NM_020098
 TESTI4024874
 TESTI4024890
 10 TESTI4024907
 TESTI4025731
 TESTI4025797
 TESTI4025920// B29 protein [Homo sapiens]// 2.00E-34// 73aa// 38%// NM_031939
 TESTI4026079
 15 TESTI4026192
 TESTI4026295
 TESTI4026456
 TESTI4026510// RNA helicase [Homo sapiens]// 0// 445aa// 89%// NM_016130
 TESTI4026524// Chromodomain helicase-DNA-binding protein 4 (CHD-4) (Mi-2 autoantigen 218 kDa protein) (Mi2-beta). // 0// 388aa// 59%// Q14839
 20 TESTI4026700
 TESTI4026762
 TESTI4026785
 TESTI4027516
 25 TESTI4027557// Galectin-9 (HOM-HD-21) (Ecalectin). // 1.00E-176// 306aa// 86%// 000182
 TESTI4027821
 TESTI4028059// 6-phosphofructokinase, muscle type (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (Phosphofructo-1-kinase isozyme A) (PFK-A). // 0// 450aa// 96%// P08237
 30 TESTI4028062
 TESTI4028429// Eppin precursor. // 2.00E-32// 61aa// 76%// 095925
 TESTI4028612
 TESTI4028809
 35 TESTI4028823// Niemann-Pick C1 protein precursor. // 6.00E-22// 127aa// 22%// P56941

- TESTI4028880// Glucose transporter type 3, brain.// 0// 436aa// 88%// P11169
 TESTI4028983
 TESTI4029370
 TESTI4029671
- 5 TESTI4029836// Potential phospholipid-transporting ATPase IB (EC 3.6.3.13).//
 0// 888aa// 93%// P98200
 TESTI4030069// fer-1 (C.elegans)-like 3 (myoferlin); fer-1 (C. elegans)-like
 3 [Homo sapiens]// 4.00E-22// 64aa// 38%// NM_013451
 TESTI4030159
- 10 TESTI4030505
 TESTI4030603
 TESTI4030669
 TESTI4032895
 TESTI4033433
- 15 TESTI4033690
 TESTI4034172
 TESTI4034212
 TESTI4034432
 TESTI4034632// polypeptide N-acetylgalactosaminyltransferase 9; UDP-GalNAc:
 20 polypeptide N-acetylgalactosaminyltransferase 9; GalNAc transferase 9;
 protein-UDP acetylgalactosaminyltransferase 9 [Homo sapiens]// 1.00E-113//
 182aa// 60%// NM_021808
 TESTI4034912// Intracellular protein transport protein US01.// 6.00E-38//
 219aa// 21%// P25386
- 25 TESTI4035063// Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170)
 (Reed- Sternberg intermediate filament associated protein).// 1.00E-17//
 72aa// 27%// P30622
 TESTI4035065
 TESTI4035498// Septin-like protein KIAA0202 (Fragment).// 7.00E-58// 112aa//
 30 49%// Q92599
 TESTI4035602
 TESTI4035637
 TESTI4035649
 TESTI4036042
- 35 TESTI4036909// Regulator of nonsense transcripts 1 homolog.// 9.00E-50//
 140aa// 32%// Q9FJRO

TESTI4037066
TESTI4037156// WHSC2 protein [Homo sapiens]// 0// 425aa// 80%// NM_005663
TESTI4037188
TESTI4037244
5 TESTI4037727// Dynein beta chain, ciliary.// 0// 573aa// 73%// P39057
TESTI4038156
TESTI4038223
TESTI4038258
TESTI4038339
10 TESTI4038492
TESTI4038818
TESTI4039038
TESTI4039086
TESTI4039659// DnaJ homolog subfamily B member 8 (mDJ6).// 1.00E-91// 165aa//
15 71%// Q9QYI7
TESTI4040363// Surfeit locus protein 5.// 3.00E-62// 120aa// 100%// Q15528
TESTI4040800
TESTI4040939
TESTI4040956
20 TESTI4041053
TESTI4041099
TESTI4041143
TESTI4041519
TESTI4041624
25 TESTI4041903
TESTI4041954
TESTI4042098
TESTI4042444
TESTI4042711
30 TESTI4043129
TESTI4043203
TESTI4043551
TESTI4043947
TESTI4044035
35 TESTI4044084
TESTI4044123

- TESTI4044186// leucine-rich, glioma inactivated 1 [Mus musculus]// 6.00E-65//
110aa// 60%// NM_020278
- TESTI4044234
- TESTI4044296
- 5 TESTI4044682
- TESTI4045312
- TESTI4046253
- TESTI4046282
- TESTI4046487// plexin 1 [Mus musculus]// 0// 433aa// 97%// NM_008881
- 10 TESTI4046819// Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase).// 4.00E-12// 134aa// 21%//
P08640
- TESTI4046884
- TESTI4047069
- 15 THYMU1000496// KINESIN-LIKE PROTEIN KIF1C.// 6.40E-61// 210aa// 53%// 043896
- THYMU1000600
- THYMU2000932
- THYMU2001053
- THYMU2001090
- 20 THYMU2003397
- THYMU2003632
- THYMU2003760
- THYMU2004693
- THYMU2005003
- 25 THYMU2005190
- THYMU2005303// T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2).// 4.2E-56// 111aa// 100%//
P01732
- THYMU2005321
- 30 THYMU2006420// TRANSCRIPTION FACTOR-LIKE PROTEIN MRGX (KIAA0026).// 2.00E-
129// 268aa// 92%// Q15014
- THYMU2007060// Mus musculus Cdc42 GTPase-activating protein mRNA, complete
cds.// 1.50E-37// 270aa// 40%// AF151363
- THYMU2007179
- 35 THYMU2007658
- THYMU2008282

- THYMU2008725// PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.1.3.48) (R-PTP- BETA).// 5.90E-192// 358aa// 98%// P23467
- THYMU2009134
- 5 THYMU2009157// Mus musculus MRPS18b mRNA for mitochondrial ribosomal protein S18b, complete cds.// 5.00E-38// 97aa// 77%// AB049954
- THYMU2009425// OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07J.// 4.90E-46// 173aa// 53%// P30954
- THYMU2011548// olfactory receptor 67 [Mus musculus]// 2.50E-56// 307aa// 39%// NP_038647
- 10 THYMU2011736// latent transforming growth factor beta binding protein 3// 0// 200aa// 99%// NP_066548
- THYMU2013386// COTE1 PROTEIN.// 2.50E-25// 269aa// 28%// P81408
- THYMU2014353
- THYMU2016204
- 15 THYMU2016523
- THYMU2019210// HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN PRECURSOR.// 2.1E-195// 248aa// 100%// Q04826
- THYMU2019587
- 20 THYMU2023711// Homo sapiens mRNA for immunoglobulin lambda heavy chain.// 2.50E-233// 477aa// 89%// Y14737
- THYMU2023967
- THYMU2025707
- THYMU2027497// 5-HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN-GATED ION CHANNEL RECEPTOR) (5-HT3R).// 2E-10// 186aa// 24%// P46098
- 25 THYMU2027695// Ig gamma-1 chain C region.// 1.00E-169// 295aa// 78%// P01857
- THYMU2027734// Homo sapiens SA hypertension-associated homolog (rat) (SAH), mRNA.// 2.00E-39// 72aa// 42%// NM_005622
- THYMU2028978
- THYMU2029676
- 30 THYMU2029688
- THYMU2030068
- THYMU2030226
- THYMU2030264
- THYMU2030637
- 35 THYMU2030796
- THYMU2031046// Copine III.// 4.00E-28// 60aa// 75%// 075131

THYMU2031218
 THYMU2031258// Homo sapiens oxysterol-binding protein-related protein (ORP1)
 mRNA, complete cds.// 4.0E-45// 125aa// 64%// AF274714
 THYMU2031341
 5 THYMU2031368
 THYMU2031579
 THYMU2031847
 THYMU2031890
 THYMU2032014// src homology 3 domain-containing protein HIP-55; HIP-55
 10 protein [Homo sapiens]// 2.00E-84// 147aa// 90%// NM_014063
 THYMU2032035
 THYMU2032080
 THYMU2032358
 THYMU2032437
 15 THYMU2032655
 THYMU2032696
 THYMU2032825// Mus musculus mRNA for Drctnnb1a, complete cds.// 2.3E-74//
 202aa// 71%// AB030242
 THYMU2033070
 20 THYMU2033079// ATP-binding cassette protein [Mus musculus].// 2.00E-53//
 105aa// 91%// AAF31421
 THYMU2033104// nuclear prelamin A recognition factor, isoform a [Homo
 sapiens]// 5.00E-34// 111aa// 47%// NP_036468
 THYMU2033308
 25 THYMU2033787
 THYMU2033816
 THYMU2034314
 THYMU2034374// Homo sapiens MAID protein mRNA, complete cds.// 1.5E-75//
 146aa// 100%// AF113535
 30 THYMU2034647
 THYMU2035064
 THYMU2035101
 THYMU2035319// Homo sapiens RNA-binding region (RNP1, RRM) containing 2
 (RNPC2)// 0// 354aa// 81%// NM_004902
 35 THYMU2035388
 THYMU2035400

- THYMU2035735// *Oryctolagus cuniculus* sarcolemmal associated protein-3 mRNA, complete cds.// 3.6E-154// 350aa// 90%// U21157
- THYMU2036058
- THYMU2036085
- 5 THYMU2036252
- THYMU2036265
- THYMU2036459// 240 KDA PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY
- 10 SUBUNIT)].// 1.40E-13// 527aa// 24%// Q28181
- THYMU2036653
- THYMU2037081
- THYMU2037208
- THYMU2037226
- 15 THYMU2037233// RNA polymerase I transcription factor RRN3 [*Homo sapiens*]// 1.00E-71// 143aa// 95%// NP_060897
- THYMU2037348
- THYMU2037965
- THYMU2038189
- 20 THYMU2038301// *Homo sapiens* mRNA for PRP8 protein, complete cds.// 3.90E-52// 112aa// 98%// AB007510
- THYMU2038369// *Mus musculus* GTRGE022 (*Gtrgeo22*) mRNA, complete cds.// 1.10E-111// 262aa// 83%// AF303106
- THYMU2038615
- 25 THYMU2038636
- THYMU2038739
- THYMU2038772
- THYMU2038797// B locus C type Lectin [*Gallus gallus*]// 2.90E-15// 147aa// 34%// CAA18961
- 30 THYMU2039305// 70 KDA WD-REPEAT TUMOR-SPECIFIC ANTIGEN (FRAGMENT).// 6.90E-40// 98aa// 83%// 035828
- THYMU2039315// *Caenorhabditis elegans* LIN-9L (*lin-9*) mRNA, complete cds.// 8.70E-66// 444aa// 34%// AF269693
- THYMU2039350
- 35 THYMU2039411
- THYMU2039780

THYMU2039989
 THYMU2040140
 THYMU2040412
 THYMU2040824
 5 THYMU2040975// PTB-ASSOCIATED SPLICING FACTOR (PSF).// 1.30E-08// 119aa//
 36%// P23246
 THYMU2041007
 THYMU2041015// Monocarboxylate transporter 8 (MCT 8) (X-linked PEST-
 containing transporter) (MCT 7).// 1.00E-132// 230aa// 54%// P36021
 10 THYMU2041252
 THYMU3000028// Rat Tamm-Horsfall protein mRNA, complete cds.// 1.3E-21//
 253aa// 28%// M63510
 THYMU3000036
 THYMU3000133
 15 THYMU3000655
 THYMU3000826
 THYMU3001083// Tubulin epsilon chain (Epsilon tubulin).// 5.00E-26// 58aa//
 98%// Q9UJT0
 THYMU3001234// Dynamin 2 (EC 3.6.1.50) (Dynamin UDNM).// 1.00E-56// 108aa//
 20 90%// P39054
 THYMU3001379// 116 kDa U5 small nuclear ribonucleoprotein component (U5
 snRNP- specific protein, 116 kDa) (U5-116 kDa).// 0// 492aa// 100%// Q15029
 THYMU3001472
 THYMU3001991// ART-4 protein [Homo sapiens]// 2.00E-46// 88aa// 97%//
 25 NM_014062
 THYMU3002452
 THYMU3002661
 THYMU3003212// *Saccharomyces cerevisiae* TAD2 gene for tRNA-specific
 adenosine-34 deaminase subunit Tad2p.// 1.10E-21// 135aa// 40%// AJ242667
 30 THYMU3003309// putative tumor antigen [Homo sapiens]// 2.00E-52// 105aa//
 66%// NM_018666
 THYMU3003763
 THYMU3004157// peroxisomal acyl-CoA thioesterase [Homo sapiens]// 3.00E-44//
 85aa// 82%// NM_005469
 35 THYMU3004835// Probable beta-1,3-galactosyltransferase 8 (EC 2.4.1.-) (Beta-
 1,3- GalTase 8) (Beta3Gal-T8) (b3Gal-T8) (UDP-galactose:beta-N-

- acetylglucosamine beta-1,3-galactosyltransferase 8) (UDP-Gal:beta- GlcNAc
beta-1,3-galactosyltransferase 8) (Beta-3-Gx-T8).// 2.00E-78// 146aa// 43%//
Q9Y2A9
- THYMU3004866// TPA inducible gene-1; TPA inducible protein [Homo sapiens]//
5 3.00E-47// 93aa// 86%// NM_015889
- THYMU3005696
- THYMU3006118// molybdenum cofactor synthesis 2 [Homo sapiens]// 3.00E-60//
112aa// 100%// NM_004531
- THYMU3006132
- 10 THYMU3006168
- THYMU3006172// membrane bound C2 domain containing protein [Rattus
norvegicus]// 1.00E-145// 460aa// 52%// NP_058945
- THYMU3006371
- THYMU3006485
- 15 THYMU3006811// ATP-binding cassette, sub-family A, member 7, isoform a//
3.00E-11// 82aa// 41%// NP_061985
- THYMU3006963
- THYMU3007137// Interleukin-16 precursor (IL-16) (Lymphocyte chemoattractant
factor) (LCF).// 0// 528aa// 83%// Q14005
- 20 THYMU3007368
- THYMU3007845
- THYMU3008171
- THYMU3008436// 6-phosphofructokinase, muscle type (EC 2.7.1.11)
(Phosphofructokinase 1) (Phosphohexokinase) (Phosphofructo-1-kinase isozyme
A) (PFK-A).// 0// 764aa// 98%// P08237
- 25 THYMU3009255
- TKIDN2000701// ankyrin G // 1.6E-90// 178aa// 100%// AAA64834
- TKIDN2002424
- TKIDN2002632
- 30 TKIDN2003044
- TKIDN2004386
- TKIDN2005934
- TKIDN2005947
- TKIDN2006525
- 35 TKIDN2006852// Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma)
mRNA, complete cds.// 4.3E-103// 192aa// 100%// AF065214

TKIDN2007667
 TKIDN2009092
 TKIDN2009641
 TKIDN2009889
 5 TKIDN2010934
 TKIDN2012824
 TKIDN2013287
 TKIDN2014757
 TKIDN2014771
 10 TKIDN2015263
 TKIDN2015788
 TKIDN2016309
 TKIDN2019116
 TLIVE2000023
 15 TLIVE2001327// Human DOCK180 protein mRNA, complete cds.// 0// 961aa// 63%//
 D50857
 TLIVE2001828
 TLIVE2001927
 TLIVE2002336// ectonucleotide pyrophosphatase/phosphodiesterase 5 [Mus
 20 musculus]// 7.00E-69// 144aa// 36%// NM_032003
 TLIVE2002338
 TLIVE2002690
 TLIVE2003197
 TLIVE2003225// CUB and Sushi multiple domains 1 [Homo sapiens]// 1.00E-129//
 25 199aa// 58%// NM_033225
 TLIVE2003381// taste receptor, type 1, member 3; saccharin preference [Mus
 musculus]// 8.00E-65// 112aa// 79%// NM_031872
 TLIVE2003970
 TLIVE2004110
 30 TLIVE2004320// Homo sapiens PC2-glutamine-rich-associated protein (PCQAP)
 mRNA, complete cds.// 4.7E-201// 368aa// 99%// AF328769
 TLIVE2004601
 TLIVE2005180
 TLIVE2006236
 35 TLIVE2006529
 TLIVE2007132

TLIVE2007528
TLIVE2007816
TLIVE2008083
TLIVE2008229// SIGNAL RECOGNITION PARTICLE 68 KDA PROTEIN (SRP68).// 1.00E-
5 299// 506aa// 96%// Q00004
TLIVE2009541
TOVAR2000649
TOVAR2001281
TOVAR2001730
10 TOVAR2002247// Homo sapiens partial partial mRNA for NICE-4 protein, clone
3114f17.// 1.0E-117// 218aa// 100%// AJ243670
TOVAR2002549
TRACH1000205
TRACH2001443
15 TRACH2001549// Homo sapiens mRNA for neuropathy target esterase.// 1.10E-94//
295aa// 65%// AJ004832
TRACH2001684
TRACH2003070
TRACH2004170
20 TRACH2005066
TRACH2005811
TRACH2006049
TRACH2006387// P2Y PURINOCEPTOR 1 (ATP RECEPTOR) (P2Y1) (PURINERGIC
RECEPTOR).// 2E-56// 307aa// 36%// P49650
25 TRACH2007059// Folate hydrolase (Prostate-specific membrane antigen 1).//
2.00E-37// 127aa// 26%// Q04609
TRACH2007834
TRACH2008300
TRACH2009310// PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME
30 III (EC 2.7.1.-).// 9.40E-85// 407aa// 38%// P41951
TRACH2019248
TRACH2019473
TRACH2020525
TRACH2021398
35 TRACH2021964
TRACH2022042

TRACH2022425// Ig alpha-1 chain C region.// 0// 319aa// 91%// P01876
 TRACH2022553// Human germline IgD-chain gene, C-region, second domain of
 membrane terminus.// 1.70E-234// 429aa// 99%// K02882
 TRACH2022649// Ig gamma-1 chain C region.// 0// 315aa// 95%// P01857
 5 TRACH2023299// growth factor receptor bound protein 2-associated protein 2
 [Mus musculus]// 5.00E-40// 77aa// 58%// NM_010248
 TRACH2023306
 TRACH2025344
 TRACH2025507// tumor suppressing subtransferable candidate 1: tumor-
 10 supressing STF cDNA 1 [Homo sapiens]// 4.00E-48// 87aa// 74%// NM_003310
 TRACH2025535// evecin-2 [Mus musculus]// 2.00E-75// 230aa// 90%// AAF01332
 TRACH2025749
 TRACH2025911
 TRACH2025932
 15 TRACH3000014
 TRACH3000342
 TRACH3000558// CREB-BINDING PROTEIN.// 1.9E-90// 120aa// 100%// Q92793
 TRACH3000586
 TRACH3000926// cardiac morphogenesis [Mus musculus]// 0// 417aa// 63%//
 20 NM_011724
 TRACH3001427// p47 [Homo sapiens]// 2.00E-85// 167aa// 49%// NM_016143
 TRACH3002064
 TRACH3002168// Cell surface glycoprotein MUC18 precursor (Melanoma-associated
 antigen MUC18) (Melanoma-associated antigen A32) (S-endo 1 endothelial-
 25 associated antigen) (CD146 antigen) (Melanoma adhesion molecule).// 0//
 341aa// 94%// P43121
 TRACH3002192
 TRACH3002650
 TRACH3002866
 30 TRACH3002871
 TRACH3003379
 TRACH3004068
 TRACH3004537
 TRACH3004721// 80 kda MCM3-associated protein (GANP protein).// 0// 474aa//
 35 77%// 060318

- TRACH3004786// Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-receptor) (CPE-R).// 2.00E-90// 162aa// 77%// 014493
 TRACH3004840
 TRACH3005294
 5 TRACH3005479
 TRACH3005549// Ig heavy chain V region IR2 precursor.// 4.00E-47// 89aa// 61%// P01805
 TRACH3006038
 TRACH3006149
 10 TRACH3006228
 TRACH3006412// Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B// 3.00E-57// 105aa// 99%// NM_022730
 TRACH3006470
 TRACH3006889
 15 TRACH3007391
 TRACH3007479// Nedd-4-like ubiquitin-protein ligase; WW domain-containing protein 2 [Homo sapiens]// 0// 320aa// 93%// NM_007014
 TRACH3008093
 TRACH3008535
 20 TRACH3008629// Cadherin-related tumor suppressor homolog precursor (Fat protein homolog).// 6.00E-36// 143aa// 28%// Q14517
 TRACH3008713// Beta-soluble NSF attachment protein (SNAP-beta) (N-ethylmaleimide-sensitive factor attachment protein, beta) (Brain protein 147) (Fragment).// 4.00E-52// 98aa// 92%// P28663
 25 TRACH3009455// Phosphatidylinositol 3-kinase regulatory alpha subunit (PI3-kinase P85-alpha subunit) (PtdIns-3-kinase P85-alpha) (PI3K).// 0// 386aa// 95%// P27986
 TRACH3034731// Ras association (RalGDS/AF-6) domain family 2// 7.00E-56// 320aa// 40%// NP_055552
 30 TRACH3034762
 TRACH3035199// antigen identified by monoclonal antibody MRC OX-2 receptor [Rattus norvegicus]// 1.00E-86// 170aa// 51%// NM_023953
 TRACH3035235
 TRACH3035482
 35 TRACH3035526// Ig alpha-2 chain C region.// 0// 324aa// 95%// P01877

TRACH3036193// Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D (EC 2.7.7.48)].// 0// 1073aa// 69%// Q82122

5 TRACH3036207

TRACH3036309

TRACH3036456

TRACH3036609// J kappa-recombination signal binding protein (RBP-J kappa).// 1.00E-158// 271aa// 89%// P31266

10 TSTOM1000135

TSTOM2000442// Ig gamma-1 chain C region.// 1.00E-168// 292aa// 77%// P01857

TSTOM2000553// SYNAPTOTAGMIN IV.// 3.00E-08// 150aa// 28%// P40749

TSTOM2002672

TUTER1000122

15 TUTER2000425// zinc finger protein SBZF3 [Homo sapiens]// 4.00E-36// 74aa// 81%// NM_020394

TUTER2000904// Unc-119 protein homolog (Retinal protein 4) (RRG4).// 7.00E-72// 129aa// 70%// Q62885

TUTER2000916

20 TUTER2001387

TUTER2002729// D6MM5E protein [Mus musculus]// 1.00E-107// 191aa// 68%// NM_033079

UTERU1000024

UTERU1000031// G.gallus mRNA for tom-1B protein.// 2.1E-149// 535aa// 59%//

25 Y08741

UTERU1000148

UTERU1000249

UTERU1000337// Putative protein phosphatase 2C (EC 3.1.3.16) (PP2C).// 1.00E-156// 271aa// 94%// P49593

30 UTERU1000339

UTERU2000649

UTERU2001409

UTERU2002410

UTERU2002841

35 UTERU2004688

UTERU2004929

UTERU2005004
 UTERU2005621// CDC14 homolog B, isoform 2 [Homo sapiens]// 0// 423aa// 94%//
 NM_033331
 UTERU2006115// ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A
 5 LARGE CHAIN) (100 KDA COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR
 HA2/AP2 ADAPTIN ALPHA A SUBUNIT).// 9.0E-141// 268aa// 99%// P17426
 UTERU2006137
 UTERU2006568
 UTERU2007444
 10 UTERU2007520
 UTERU2007724// Calponin H2, smooth muscle (Neutral calponin).// 1.00E-144//
 253aa// 86%// Q99439
 UTERU2008347// Chlamydomonas reinhardtii vegetative cell wall protein gp1
 (GP1) gene, complete cds.// 1.0E-19// 199aa// 30%// AF309494
 15 UTERU2014678
 UTERU2017762// plexin B1; KIAA0407 protein; plexin 5 [Homo sapiens]// 0//
 383aa// 60%// NM_002673
 UTERU2019491// Homo sapiens mRNA for 41-kDa phosphoribosylpyrophosphate
 synthetase-associated protein, complete cds.// 4.30E-48// 101aa// 100%//
 20 AB007851
 UTERU2019681
 UTERU2019706// T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA) (CCT-
 GAMMA).// 9.80E-273// 426aa// 99%// P49368
 UTERU2019940// mitochondrial ribosomal protein L30 [Homo sapiens]// 2.00E-
 25 44// 82aa// 97%// NM_016503
 UTERU2020491
 UTERU2020718
 UTERU2021163
 UTERU2021380
 30 UTERU2022020
 UTERU2022981
 UTERU2023039
 UTERU2023175
 UTERU2023651
 35 UTERU2023712
 UTERU2024002

- UTERU2024656
 UTERU2025025// High affinity nerve growth factor receptor precursor (EC 2.7.1.112) (TRK1 transforming tyrosine kinase protein) (p140-TrkA) (Trk-A).// 0// 479aa// 95%// P04629
- 5 UTERU2025645
 UTERU2025891
 UTERU2026025// SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KDA) (PR264 PROTEIN).// 8.00E-30// 61aa// 100%// P30352
- 10 UTERU2026090// Cartilage-associated protein precursor.// 1.00E-180// 309aa// 87%// 075718
 UTERU2026203// phosphoinositide phosphatase SAC1 [Rattus norvegicus].// 1.00E-107// 221aa// 95%// AAG29810
 UTERU2027591// calcium-activated potassium channel // 7.8E-33// 79aa// 94%//
- 15 AAA50216
 UTERU2029953
 UTERU2030213
 UTERU2030280
 UTERU2031084
- 20 UTERU2031268// NY-REN-25 antigen [Homo sapiens].// 1.00E-41// 330aa// 49%// AAD42869
 UTERU2031521
 UTERU2031703
 UTERU2031851
- 25 UTERU2033375
 UTERU2033382
 UTERU2035114
 UTERU2035323
 UTERU2035328// Homo sapiens putative transcription factor CA150 mRNA, complete cds.// 1.80E-271// 796aa// 70%// AF017789
- 30 UTERU2035331
 UTERU2035452// NG3 [Homo sapiens]// 1.00E-136// 150aa// 99%// AAB47494
 UTERU2035469// Mus musculus microfibril-associated glycoprotein-2 (Magp2) mRNA, complete cds.// 1.2E-52// 164aa// 66%// AF180805
- 35 UTERU2035503

- UTERU2035745// MYOSIN IA HEAVY CHAIN (MYOSIN-LIKE PROTEIN ABMA).// 1.30E-11//
101aa// 31%// P22467
- UTERU2036089// SH3-BINDING PROTEIN 3BP-1.// 4.1E-168// 369aa// 86%// P55194
UTERU2037361
- 5 UTERU2037577
- UTERU2038251
- UTERU3000226
- UTERU3000645// Claudin-4 (Clostridium perfringens enterotoxin receptor) (CPE-
receptor) (CPE-R).// 3.00E-89// 161aa// 77%// 014493
- 10 UTERU3000665// Snf2-related CBP activator protein [Homo sapiens].// 7.00E-
59// 500aa// 97%// NP_006653
- UTERU3000828// 116 kDa U5 small nuclear ribonucleoprotein component (U5
snRNP- specific protein, 116 kDa) (U5-116 kDa).// 0// 931aa// 95%// Q15029
- UTERU3000899// hTGN51 [Homo sapiens].// 1.00E-101// 281aa// 72%// AAC39542
- 15 UTERU3001059// ABC1 protein homolog, mitochondrial precursor.// 2.00E-99//
188aa// 48%// Q92338
- UTERU3001240// Adenylate cyclase, type IV (EC 4.6.1.1) (ATP pyrophosphate-
lyase) (Adenylyl cyclase).// 1.00E-176// 308aa// 81%// P26770
- UTERU3001542
- 20 UTERU3001571
- UTERU3001572// Neuroblast differentiation associated protein AHNAK
(Desmoyokin) (Fragments).// 6.00E-19// 213aa// 21%// Q09666
- UTERU3001585// Cytochrome P450 4c3 (EC 1.14.-.-) (CYP1VC3).// 1.00E-125//
230aa// 49%// Q9VA27
- 25 UTERU3001652// 64 KDA AUTOANTIGEN D1 (THYROID-ASSOCIATED OPHTHALMOPATHY
AUTOANTIGEN).// 1.00E-219// 416aa// 99%// P29536
- UTERU3001766
- UTERU3001988// COATOMER EPSILON SUBUNIT (EPSILON-COAT PROTEIN) (EPSILON-
COP).// 1.70E-126// 159aa// 94%// Q28104
- 30 UTERU3002209
- UTERU3002218
- UTERU3002383
- UTERU3002667
- UTERU3002731
- 35 UTERU3002768
- UTERU3002786

UTERU3002993

UTERU3003116// ADAM 12 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 12) (Meltrin alpha).// 1.00E-20// 48aa// 44%// 043184

5 UTERU3003135// Splicing factor 3B subunit 2 (Spliceosome associated protein 145) (SAP 145) (SF3b150) (Pre-mRNA splicing factor SF3b 145 kDa subunit).// 6.00E-29// 62aa// 83%// Q13435

UTERU3003178// Kinesin light chain 2 (KLC 2).// 0// 312aa// 88%// Q9H0B6
UTERU3003465

10 UTERU3003523

UTERU3003776

UTERU3004523

UTERU3004616

UTERU3004709

15 UTERU3004992// Aortic preferentially expressed protein 1 (APEG-1).// 3.00E-61// 113aa// 100%// Q15772

UTERU3005049

UTERU3005205

UTERU3005230

20 UTERU3005460

UTERU3005585// rhophilin-like protein [Homo sapiens]// 0// 380aa// 91%// NM_033103

UTERU3005907// PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (EC 2.3.2.13) (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC) (TGASE-H).// 1.30E-75// 152aa//

25 98%// P21980

UTERU3005970

UTERU3006008

UTERU3006308// SEMAPHORIN 4C PRECURSOR (SEMAPHORIN I) // 1.00E-128// 330aa// 86%// Q64151

30 UTERU3007134

UTERU3007419// Rattus norvegicus Ca²⁺-dependent activator protein (CAPS) mRNA, complete cds.// 0// 1223aa// 78%// U16802

UTERU3007640// N-ethylmaleimide-sensitive factor attachment protein, alpha:// 5.00E-54// 110aa// 87%// NP_003818

35 UTERU3007913

UTERU3008660

- UTERU3008671// SPARC precursor (Secreted protein acidic and rich in cysteine) (Osteonectin) (ON) (Basement membrane protein BM-40).// 4.00E-25// 49aa// 96%// P09486
- UTERU3009259
- 5 UTERU3009490// LYSP100 protein (Lymphoid-restricted homolog of Sp100) (Nuclear autoantigen Sp-140) (Speckled 140 kDa) (Nuclear body protein Sp140).// 4.00E-33// 67aa// 61%// Q13342
- UTERU3009517
- 10 UTERU3009690// alpha-1A-adrenergic receptor, isoform 2: adrenergic, alpha - 1A-, receptor: adrenergic, alpha-1C-, receptor: alpha 1A-adrenoceptor [Homo sapiens]// 5.00E-16// 41aa// 67%// NM_033303
- UTERU3009871// feminization 1 homolog a (C. elegans)// 0// 588aa// 85%// NP_034322
- 15 UTERU3009979// growth arrest-specific 6: AXL stimulatory factor [Homo sapiens]// 0// 572aa// 97%// NM_000820
- UTERU3011063// Transmembrane 9 superfamily protein member 4.// 0// 402aa// 89%// Q92544
- UTERU3015086
- 20 UTERU3015500// G protein-coupled receptor 49// 1.00E-15// 350aa// 29%// NP_003658
- UTERU3016789// SH3 domain-binding protein 3BP-2.// 1.00E-146// 261aa// 75%// P78314
- UTERU3018081
- UTERU3018154
- 25 UTERU3018616
- UTERU3018711
- 3NB692004724
- ADRGL2000042// Homo sapiens CTCL tumor antigen se20-4 mRNA, complete cds.// 6.20E-143// 269aa// 100%// AF273046
- 30 ADRGL2000056
- BLADE2000579
- BLADE2006830
- BRACE2002589
- BRACE2003609// endothelial zinc finger protein induced by tumor necrosis factor alpha [Homo sapiens]// 0// 310aa// 67%// NM_021216
- 35 BRACE2009318

BRACE2011677
 BRACE2029396
 BRACE2037299
 BRACE2039823// CDP-DIACYLGLYCEROL—INOSITOL 3-PHOSPHATIDYLTRANSFERASE (EC
 5 2.7.8.11) (PHOSPHATIDYLINOSITOL SYNTHASE) (PTDINS SYNTHASE) (PI SYNTHASE).//
 2.10E-79// 154aa// 100%// 014735
 BRACE2039832
 BRACE2043105
 BRACE3001058// zinc finger protein 347; zinc finger 1111 [Homo sapiens]// 0//
 10 382aa// 52%// NM_032584
 BRACE3001113// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7).//
 6.00E-92// 226aa// 26%// Q05481
 BRACE3003026
 BRACE3003053
 15 BRACE3005107// // // // //
 BRACE3009127// oxysterol binding protein 2; oxysterol binding protein-like 1
 [Homo sapiens]// 0// 670aa// 95%// NM_030758
 BRACE3010076// Vigilin (High density lipoprotein-binding protein) (HDL-
 binding protein).// 0// 464aa// 92%// Q00341
 20 BRACE3015829
 BRACE3021148// DC12 protein [Homo sapiens]// 1.00E-16// 60aa// 30%//
 NM_020187
 BRALZ2017844// HOMEBOX PROTEIN CHOX-E (CHOX E) (FRAGMENT).// 2.80E-59//
 157aa// 75%// Q91975
 25 BRAMY2019111// POLYCYSTIN 2.// 6.30E-18// 204aa// 27%// 035245
 BRAMY2035070// Homo sapiens zinc finger 1111 mRNA, complete cds.// 1.70E-
 213// 723aa// 53%// AY029765
 BRAMY2035449// Mus musculus zinc finger protein ZFP113 mRNA, complete cds.//
 2.70E-95// 356aa// 44%// AF167320
 30 BRAMY2035718// NUCLEAR FACTOR 1-B (NFI-B) (CCAAT BOX-BINDING TRANSCRIPTION
 FACTOR) (CTF) (TGGCA-BINDING PROTEIN).// 5.60E-228// 418aa// 97%// P97863
 BRAMY2038516// PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC
 5.3.4.1).// 7.00E-237// 434aa// 99%// Q15084
 BRAMY2039341// ZINC FINGER PROTEIN 135.// 7.30E-84// 227aa// 62%// P52742
 35 BRAMY2040159// Homo sapiens MRIP-1 mRNA, complete cds.// 6.00E-234// 345aa//
 91%// AF359283

- BRAMY2041434
 BRAMY2045471// Homo sapiens CGI-89 protein mRNA, complete cds.// 6.00E-45//
 147aa// 44%// CAB82308
 BRAMY3004800// Huntingtin-associated protein-interacting protein (Duo
 5 protein).// 0// 751aa// 91%// 060229
 BRAWH1000369// Homo sapiens putative DNA polymerase mRNA, partial cds.//
 5.40E-150// 199aa// 97%// AF044578
 BRAWH2006207// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//
 8.90E-32// 83aa// 81%// Q05481
 10 BRAWH2006395// transmembrane receptor UNC5H1// 1.00E-141// 292aa// 88%//
 AAB57678
 BRAWH2008993
 BRAWH2009393
 BRAWH2010552
 15 BRAWH3007441// CAT56 protein [Homo sapiens]// 1.00E-44// 78aa// 84%//
 NM_025263
 BRAWH3009017// SEL-10 protein.// 6.00E-38// 73aa// 61%// Q93794
 BRCAN2002473// Tropomyosin, fibroblast isoform 2 (TM-2).// 1.00E-114//
 230aa// 70%// P19354
 20 BRCAN2002854// Human Hsp27 ERE-TATA-binding protein (HET) mRNA, complete
 cds.// 2.60E-21// 240aa// 35%// U72355
 BRCAN2003070// ubiquitin carrier protein E2-C [Homo sapiens]// 9.00E-51//
 80aa// 78%// NP_008950
 BRCAN2014229
 25 BRCOC2019841
 BRHIP2002722
 BRHIP2003272
 BRHIP2005271// protein tyrosine phosphatase// 7.00E-39// 190aa// 42%//
 NP_006255
 30 BRHIP2005724// Homo sapiens mRNA for NDRG4-B, complete cds.// 3.10E-182//
 301aa// 98%// AB044944
 BRHIP2006617// NUCLEAR AUTOANTIGENIC SPERM PROTEIN (NASP).// 1.20E-156//
 313aa// 97%// P49321
 BRHIP2008389// Drosophila melanogaster furry protein short isoform mRNA,
 35 partial cds.// 1.70E-29// 179aa// 44%// AF351187
 BRHIP2012360// XPG_XENLA// 4.00E-17// 70aa// 41%// P14629

- BRHIP2017553// Zinc finger protein 184.// 1.00E-164// 272aa// 49%// Q99676
 BRHIP2026877// Tyrosine-protein kinase receptor TYR03 precursor (EC
 2.7.1.112) (Tyrosine-protein kinase RSE) (Tyrosine-protein kinase SKY)
 (Tyrosine- protein kinase DTK) (Protein-tyrosine kinase byk).// 3.00E-56//
 5 104aa// 80%// Q06418
 BRHIP3000017
 BRHIP3000240// Homo sapiens potassium channel beta 2 subunit (HKvbeta2.2)
 mRNA, alternatively spliced, complete cds.// 1.70E-172// 347aa// 95%//
 AF044253
 10 BRHIP3008314// sirtuin 2, isoform 2: silencing information regulator 2-like;
 sir2-like 2: silent mating type information regulation 2, S.cerevisiae,
 homolog 2: sir2-related protein type 2 [Homo sapiens]// 2.00E-48// 86aa//
 98%// NM_030593
 BRHIP3026052// Serine/threonine protein phosphatase 2A, 56 kDa regulatory
 15 subunit, gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit,
 B56 gamma isoform) (PP2A, B subunit, PR61 gamma isoform) (PP2A, B subunit, R5
 gamma isoform).// 0// 424aa// 83%// Q13362
 BRSTN2013354// ETS-related protein PE-1 (ETS translocation variant 3)
 (Fragment).// 4.00E-61// 109aa// 84%// P41162
 20 BRTHA2002133
 BRTHA2002702
 BRTHA2007060// EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3
 THETA) (EUKARYOTIC TRANSLATION INITIATION FACTOR 3 LARGE SUBUNIT) (PNLA-
 35).// 0// 963aa// 74%// Q40554
 25 BRTHA2010033
 BRTHA2011321
 BRTHA2013426
 BRTHA2013610// deoxyguanosine kinase, putative [Arabidopsis thaliana]//
 1.00E-142// 360aa// 78%// NP_565032*
 30 BRTHA2016318// WTAP protein// 9.00E-87// 240aa// 100%// CAC10188
 BRTHA2017364// PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME
 III.// 1.10E-33// 207aa// 34%// P34580
 BRTHA2017972// Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete
 cds.// 5.30E-114// 207aa// 99%// AF010193
 35 BRTHA2018011// EPITHIN (EC 3.4.21.-).// 1.70E-53// 242aa// 45%// P56677

- BRTHA2018443// POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IS (EC 3.6.1.-)
(FRAGMENT).// 3.10E-195// 581aa// 61%// P98196
- BRTHA3000296
- BRTHA3003000// apoptosis-associated tyrosine kinase [Homo sapiens]// 1.00E-
5 161// 300aa// 64%// NM_004920
- BRTHA3008826
- CERVX2002013// TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT
BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2).// 3.30E-33// 81aa// 81%//
Q13887
- 10 CTONG1000113// ZINC FINGER PROTEIN 184 (FRAGMENT).// 0// 641aa// 85%// Q99676
- CTONG2003348// Mus musculus mRNA for OASIS protein, complete cds.// 9.60E-
87// 392aa// 51%// AB017614
- CTONG2004000
- CTONG2008721// Homo sapiens CAGH44 mRNA, partial cds.// 2.70E-94// 215aa//
15 91%// U80741
- CTONG2015596
- CTONG2015633
- CTONG2016942// Homo sapiens serine protease DESC1 (DESC1) mRNA, complete
cds.// 2.00E-95// 425aa// 43%// AF064819
- 20 CTONG2019822
- CTONG2020374
- CTONG2020378// ZINC FINGER PROTEIN 35 (ZFP-35).// 5.70E-100// 322aa// 55%//
P15620
- CTONG2020411// BASONUCLIN.// 1.30E-139// 616aa// 48%// Q01954
- 25 CTONG2020974// Homo sapiens mRNA for putative progesterone binding protein.//
8.10E-118// 223aa// 100%// AJ002030
- CTONG2024031
- CTONG2028758// Mus musculus zfh-4 mRNA for zinc-finger homeodomain protein 4,
complete cds.// 0// 907aa// 91%// AB024499
- 30 CTONG3001501// Mus musculus glucocorticoid-induced gene 1 mRNA, complete
cds.// 3.60E-202// 413aa// 89%// AF292939
- CTONG3002552
- CTONG300359°
- CTONG3004550// SH3-domain binding protein 4 [Homo sapiens]// 1.00E-179//
35 351aa// 42%// NM_014521

- CTONG3004726// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//
4.20E-230// 663aa// 55%// Q05481
- CTONG3009287
- DFNES2011192// Homo sapiens ZNF140-like transcription factor mRNA, complete
5 cds.// 1.10E-221// 396aa// 99%// AF326206
- FCBBF1000509// Homo sapiens mRNA for photolyase, complete cds.// 9.80E-280//
500aa// 99%// D83702
- FCBBF3010361// Danio rerio mRNA for winged helix nude (whn gene).// 2.10E-
107// 336aa// 64%// AJ252024
- 10 FCBBF3027854// contains similarity to Arabidopsis thaliana DNA-damage-
repair/tolerance resistance protein DRT111 (SW:P42698// 9.60E-12// 87aa//
37%// AAC13593
- FEBRA2000790
- FEBRA2001990// SON OF SEVENLESS PROTEIN HOMOLOG 2 (SOS-2) (MSOS-2)
15 (FRAGMENT).// 4.00E-09// 175aa// 20%// Q02384
- FEBRA2006519// Mus musculus papilin mRNA, complete cds.// 4.90E-58// 327aa//
37%// AF314171
- FEBRA2008692// Homo sapiens IRE1b mRNA for protein kinase/ribonuclease IRE1
beta, complete cds.// 0// 926aa// 96%// AB047079
- 20 FEBRA2014122// wizL [Mus musculus]// 0// 661aa// 88%// BAA32790
- FEBRA2027609// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//
5.60E-196// 688aa// 51%// Q05481
- FEBRA2028256// FIBRILLIN 2 PRECURSOR.// 2.90E-231// 527aa// 62%// Q61555
- FEBRA2028516
- 25 HCASM2002754
- HCASM2003018// Homo sapiens nuclear transcription factor NFX2 (NFX2) mRNA,
complete cds.// 3.90E-70// 666aa// 31%// AF332009
- HCASM2003099// HISTONE DEACETYLASE CLR3.// 5.00E-19// 108aa// 49%// P56523
- HCASM2003357
- 30 HCASM2008536// DNA-REPAIR PROTEIN XRCC1.// 2.00E-12// 119aa// 36%// P18887
- HCASM2009424// regulatory factor (trans-acting) 2 [Mus musculus]// 7.00E-24//
60aa// 48%// NP_033082
- HCHON2000508// Homo sapiens prostate antigen PARIS-1 mRNA, complete cds.//
0// 686aa// 99%// AY026527
- 35 HCHON2000743

- HCHON2004858// Zinc finger protein 29 (Zfp-29).// 1.00E-124// 208aa// 60%// Q07230
- HEART2009680// Vasoactive intestinal polypeptide receptor 2 precursor (VIP-R-2) (Pituitary adenylate cyclase activating polypeptide type III receptor) (PACAP type III receptor) (PACAP-R-3) (Helodermin-preferring VIP receptor).// 0// 309aa// 96%// P41587
- 5 HLUNG2013350// Mus musculus mRNA for synaptotagmin VIII, complete cds.// 1.70E-39// 126aa// 67%// AB026805
- HLUNG2015418// similar to cadherin and Drosophila Fat protein; similar to
- 10 CAA60685 (PID:g1107687) [Homo sapiens].// 1.00E-139// 500aa// 91%// AAD28068
- HLUNG2015548// INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (EC 1.1.1.205) (IMP DEHYDROGENASE 1) (IMPDH-I) (IMPD 1).// 3.30E-253// 521aa// 94%// P20839
- HLUNG2016862
- HSYRA2005628// ZINC FINGER PROTEIN 195.// 1.30E-237// 426aa// 78%// 014628
- 15 IMR322001879
- IMR322007078
- IMR322008651// DNA REPAIR PROTEIN RAD51 HOMOLOG 1.// 8.40E-154// 340aa// 89%// Q06609
- IMR322013396// Homo sapiens cone photoreceptor cGMP-gated channel alpha
- 20 subunit (CNGA3) mRNA, complete cds.// 0// 638aa// 98%// AF065314
- IMR322013731// TAT-BINDING HOMOLOG 7.// 1.90E-74// 187aa// 47%// P54816
- LIVER2000247// RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).// 2.70E-57// 243aa// 48%// Q13183
- MESAN2001770// EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA)
- 25 (EIF- 4G) (EIF4G) (P220).// 4.70E-185// 420aa// 86%// Q04637
- MESAN2005303// DNA BINDING PROTEIN URE-B1 (EC 6.3.2.-).// 2.80E-36// 171aa// 46%// P51593
- MESAN2014412// Mus musculus zfh-4 mRNA for zinc-finger homeodomain protein 4, complete cds.// 2.8e-317// 606aa// 92%// AB024499
- 30 MESAN2015501// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).// 7.80E-222// 753aa// 52%// Q05481
- NT2R12005772// Rattus norvegicus mRNA for DLG6 alpha, complete cds.// 4.30E-176// 273aa// 75%// AB030499
- NT2R12008952// ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).// 1.40E-
- 35 131// 393aa// 55%// P51523

- NT2R12009583// Homo sapiens orphan G-protein coupled receptor (GPC5C) mRNA, complete cds.// 3.70E-241// 441aa// 100%// AF207989
- NT2R12018448// AE-binding protein 2 [Mus musculus]// 1.00E-153// 258aa// 92%// NM_009637
- 5 NT2R12027157// Mouse SDR2 mRNA, complete cds.// 3.20E-233// 539aa// 77%// D50464
- NT2R13000174// Homo sapiens HepA-related protein HARP mRNA, complete cds.// 1.00E-38// 136aa// 46%// NP_054859.1
- NT2R13001132// Mus musculus Arkadia (Arkadia) mRNA, complete cds.// 0// 994aa// 90%// AF330197
- 10 NT2R13002557
- NT2R13005928
- NT2R13007167
- NT2R13007443// MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 5 (EC 2.7.1.-) (MAPK/ERK KINASE KINASE 5) (MEK KINASE 5) (MEKK 5) (APOPTOSIS SIGNAL-REGULATING KINASE 1) (ASK-1).// 9.50E-244// 606aa// 66%// Q99683
- 15 NT2RP7008435// EPITHIN (EC 3.4.21.-).// 6.60E-79// 354aa// 43%// P56677
- NT2RP8000521
- NTONG2008093// 6PF-2-K/FRU-2, 6-P2ASE BRAIN/PLACENTA-TYPE ISOZYME [INCLUDES: 6- PHOSPHOFRUCTO-2-KINASE (EC 2.7.1.105); FRUCTOSE-2,6-BISPHOSPHATASE (EC 3.1.3.46)].// 1.60E-72// 143aa// 97%// Q16875
- 20 OCBBF2003327// ADAM-TS 6 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 6) (ADAMTS-6) (ADAM-TS6).// 2.00E-63// 108aa// 51%// Q9UKP5
- 25 OCBBF2005433// N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).// 7.70E-24// 213aa// 33%// P30337
- OCBBF2006987
- OCBBF2008144// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).// 5.50E-244// 757aa// 56%// Q05481
- 30 OCBBF2009583// ZINC FINGER PROTEIN 184 (FRAGMENT).// 1.20E-75// 345aa// 36%// Q99676
- OCBBF2011669// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7).// 1.00E-90// 222aa// 26%// Q05481
- OCBBF2019684// ZINC FINGER PROTEIN 29 (ZFP-29).// 6.90E-246// 465aa// 90%// Q07230
- 35

- OCBBF2020048// 95 kDa retinoblastoma protein binding protein; KIAA0661 gene product // 9.90E-97// 339aa// 63%// XP_010492
- OCBBF2024284// GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 (P205) (RECEPTOR OF ACTIVATED PROTEIN KINASE C 1) (RACK1).// 1.60E-72//
- 5 135aa// 99%// P25388
- OCBBF2030116
- OCBBF2032274// Zinc finger protein 93 (Zinc finger protein HTF34) (Fragment).// 1.00E-145// 247aa// 67%// P35789
- OCBBF2034637// microtubule associated testis specific serine/threonine
- 10 protein kinase [Mus musculus]// 0// 450aa// 79%// NP_032667
- OCBBF3000167// ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).// 5.00E-156// 405aa// 62%// P51522
- OCBBF3002654// Triple functional domain protein (PTPRF interacting protein).// 0// 510aa// 93%// 075962
- 15 OCBBF3003761
- OCBBF3004972
- PERIC2007068// Mus musculus mRNA for 1A13 protein.// 3.30E-121// 385aa// 62%// X83587
- PLACE7000333
- 20 PLACE7000502// Human Notch4 (hNotch4) mRNA, complete cds.// 0// 666aa// 99%// U95299
- PROST2000452// TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).// 1.60E-47// 186aa// 50%// 015393
- PROST2009320// enigma protein; LIM domain protein [Homo sapiens]// 6.00E-42//
- 25 77aa// 71%// NM_005451
- PROST2019487
- PUAEN2006335
- SKMUS2003194
- SPLEN2004611// Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2).// 1.00E-19// 50aa// 47%// NM_030756
- 30 SPLEN2016135// Zinc finger protein 2 (Zfp-2) (mKR2 protein).// 6.00E-27// 64aa// 39%// P08043
- SPLEN2016781// zinc finger transcription factor REST protein // 5.00E-18// 80aa// 33%// AAB94893
- 35 SPLEN2016932

- SPLEN2030847// Mus musculus Kif21b (Kif21b) mRNA, complete cds.// 1.00E-85// 110aa// 94%// AF202893
- SPLEN2033490
- SPLEN2036702// TENSIN.// 8.30E-175// 409aa// 54%// Q04205
- 5 SPLEN2037319
- SPLEN2039311// Pro-Pol-dUTPasepolyprotein.*// 2.70E-15// 93aa// 53%// 002711*
- SPLEN2039379// Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds.// 0// 645aa// 99%// AF012872
- 10 STOMA2003158// DEOXYRIBONUCLEASE GAMMA PRECURSOR (EC 3.1.21.-) (DNASE GAMMA) (DEOXYRIBONUCLEASE I-LIKE 3) (DNASE I HOMOLOGOUS PROTEIN DHP2) (LIVER AND SPLEEN DNASE) (LS-DNASE) (LSD).// 5.40E-143// 267aa// 99%// Q13609
- STOMA2004893
- SYNOV1000256// Human preferentially expressed antigen of melanoma (PRAME) mRNA, complete cds.// 2.80E-29// 275aa// 35%// U65011
- 15 SYNOV2001660
- SYNOV2006620
- SYNOV2013637// Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds.// 2.40E-54// 213aa// 53%// AF057039
- SYNOV2021953// hematopoietic zinc finger [Mus musculus]// 1.00E-63// 300aa// 51%// NP_038894
- 20 SYNOV4002744// Zinc finger protein 84 (Zinc finger protein HPF2).// 2.00E-26// 75aa// 30%// P51523
- SYNOV4003981// megakaryocyte stimulating factor [Homo sapiens]// 0// 400aa// 74%// NM_005807
- 25 SYNOV4005739
- SYNOV4005889
- TBAES2000932// sirtuin 7; sirtuin type 7; silent mating type information regulation 2, S.cerevisiae, homolog 7; sir2-related protein type 7 [Homo sapiens]// 1.00E-69// 120aa// 93%// NM_016538
- 30 TESOP2000390// Mitogen-activated protein kinase kinase kinase 14 (EC 2.7.1.37) (NF-kappa beta-inducing kinase) (Serine/threonine protein kinase NIK) (HsNIK).// 0// 354aa// 81%// Q99558
- TESOP2001796// RING finger protein 19 (Dorfin) (Double ring-finger protein) (p38 protein).// 0// 320aa// 69%// Q9NV58
- 35 TESOP2005199// ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).// 8.40E-104// 317aa// 49%// P17097

- TESOP2006398// zinc finger-like; similar to P52742 (PID:g1731411) [Homo sapiens].// 4.00E-22// 100aa// 97%// AAC36300
- TESOP2006865// ZINC FINGER PROTEIN MFG-3.// 5.30E-29// 116aa// 55%// P16374
- TESOP2007384// Mus musculus putative purine nucleotide binding protein mRNA,
 5 complete cds.// 1.00E-78// 288aa// 55%// U44731
- TESTI1000266
- TESTI2008901
- TESTI2015626// Human mRNA for phosphoribosypyrophosphate synthetase-associated protein 39, complete cds.// 1.00E-181// 356aa// 99%// D61391
- 10 TESTI2025924// CASEIN KINASE I, EPSILON ISOFORM (EC 2.7.1.-) (CKI-EPSILON).// 1.80E-42// 265aa// 36%// P49674
- TESTI2026647// PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10).// 6.40E-48// 226aa// 45%// Q13206
- TESTI2029252// Homo sapiens mRNA for LAK-4p, complete cds.// 2.40E-79//
 15 410aa// 38%// AB002405
- TESTI2032643// ADENYLATE CYCLASE, TYPE IV (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).// 1.00E-176// 155aa// 75%// P26770
- TESTI2034251// ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).// 3.10E-186// 546aa// 57%// Q05481
- 20 TESTI2035981
- TESTI2036288// PROSTAGLANDIN-F SYNTHASE 1 (EC 1.1.1.188) (PGF SYNTHASE 1) (PGF 1) (PROSTAGLANDIN-D2 11 REDUCTASE 1) (PGFS1).// 1.10E-41// 120aa// 69%// P05980
- TESTI2037830
- 25 TESTI2039060// MALTASE-GLUCOAMYLASE, INTESTINAL [INCLUDES: MALTASE (EC 3.2.1.20) (ALPHA-GLUCOSIDASE); GLUCOAMYLASE (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)].// 8.60E-287// 641aa// 77%// 043451
- TESTI2049956// Vegetatible incompatibility protein HET-E-1.// 5.00E-43// 107aa// 34%// Q00808
- 30 TESTI2050780// organic anion transporter OATP-E [Homo sapiens]// 4.00E-28// 71aa// 34%// NM_016354
- TESTI4000137
- TESTI4000155
- TESTI4000183// ZINC FINGER PROTEIN 177.// 4.60E-66// 299aa// 43%// Q13360
- 35 TESTI4000214// similar to human transcription factor TFIIS (S34159)// 7.00E-40// 400aa// 32%// BAA13438

- TESTI4000319// GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF).// 4.70E-50// 256aa// 48%// Q03386
- TESTI4001984
- 5 TESTI4005317// Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA// 0// 536aa// 95%// NM_012197
- TESTI4006473// ATP-dependent RNA helicase A (Nuclear DNA helicase II) (NDH II) (DEAD-box protein 9).// 5.00E-72// 208aa// 33%// Q28141
- TESTI4008058
- 10 TESTI4008302// zinc finger protein [Homo sapiens]// 0// 382aa// 89%// NM_014347
- TESTI4010382// cytoplasmic dynein heavy chain 2 [Rattus norvegicus]// 0// 1171aa// 90%// NM_023024
- TESTI4011070// Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase).// 5.00E-18// 148aa// 20%//
- 15 P08640
- TESTI4011072// tudor domain containing 1 [Mus musculus]// 1.00E-38// 201aa// 22%// NM_031387
- TESTI4011829
- TESTI4013365// S-antigen protein precursor.// 6.00E-07// 109aa// 20%// Q03400
- 20 TESTI4013602
- TESTI4013894// mitsugumin 29 [Mus musculus]// 1.00E-117// 200aa// 92%// NM_008596
- TESTI4014801// novel protein similar to archaeal, yeast and worm N2, N2-dimethylguanosine tRNA methyltransferase [Homo sapiens]// 0// 312aa// 89%//
- 25 NM_030934
- TESTI4015012
- TESTI4015442// zinc finger homeodomain 4 [Mus musculus]// 0// 875aa// 79%// NM_030708
- TESTI4017714// Protease II (EC 3.4.21.83) (Oligopeptidase B).// 4.00E-52//
- 30 175aa// 25%// Q59536
- TESTI4019657// cyclin G associated kinase [Homo sapiens]// 1.00E-138// 311aa// 88%// NP_005246
- TESTI4021482// RAC-alpha serine/threonine kinase (EC 2.7.1.-) (RAC-PK-alpha) (Protein kinase B) (PKB) (C-AKT).// 3.00E-28// 58aa// 98%// P31749
- 35 TESTI4024387// RAB GDP dissociation inhibitor alpha (RAB GDI alpha) (GDI-1).// 1.00E-102// 179aa// 98%// P50398

- TESTI4025268// 77 kDa echinoderm microtubule-associated protein.// 1.00E-45//
119aa// 31%// Q26613
- TESTI4025494// Zinc finger protein 33A (Zinc finger protein KOX31)
(HA0946).// 0// 384aa// 49%// Q06730
- 5 TESTI4025547// double-stranded RNA-binding zinc finger protein JAZ [Homo
sapiens]// 1.00E-161// 279aa// 87%// NM_012279
- TESTI4025865
- TESTI4026207// Kinesin-like protein KLP1.// 1.00E-83// 167aa// 43%// P46870
- TESTI4028938// Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1).//
10 0// 373aa// 66%// Q03923
- TESTI4028958
- TESTI4029348
- TESTI4029528
- TESTI4029690
- 15 TESTI4031745// Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.1.-)
(MAPK/ERK kinase kinase 5) (MEK kinase 5) (MEKK 5) (Apoptosis signal-
regulating kinase 1) (ASK-1).// 0// 447aa// 58%// Q99683
- TESTI4032090
- TESTI4032112// Homo sapiens general transcription factor IIIC, polypeptide 1
20 (alpha subunit, 220kD) (GTF3C1), mRNA// 1.00E-121// 213aa// 82%// NM_001520
- TESTI4036767
- TESTI4038721
- TESTI4041086
- TESTI4046240// sirtuin 7// 1.00E-115// 44aa// 98%// NP_057622
- 25 THYMU2004139// WEE1-LIKE PROTEIN KINASE (EC 2.7.1.112).// 2.80E-137// 534aa//
54%// P47817
- THYMU2004284// UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).// 9.00E-63//
122aa// 100%// P22314
- THYMU2006001// ZINC-BINDING PROTEIN A33.// 8.40E-51// 476aa// 27%// Q02084
- 30 THYMU2028739// ZINC FINGER PROTEIN 263 (ZINC FINGER PROTEIN FPM315).// 1.10E-
39// 291aa// 40%// 014978
- THYMU2030462
- THYMU2031139// Homo sapiens zinc metalloprotease ADAMTS7 (ADAMTS7) mRNA,
complete cds.// 3.30E-105// 504aa// 42%// AF140675
- 35 THYMU2031249// SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (EC 2.7.1.-).//
1.20E-138// 291aa// 92%// Q00536

- THYMU2032976
 THYMU2033401
 THYMU2034279
 THYMU2035078// LRP16 protein [Homo sapiens]// 3.00E-50// 80aa// 55%//
 5 NP_054786
 THYMU2035710// Tyrosine-protein kinase-like 7 [Precursor]// 1.00E-50//
 121aa// 80%// Q13308
 THYMU2040925// CDP-DIACYLGLYCEROL—INOSITOL 3-PHOSPHATIDYLTRANSFERASE (EC
 2.7.8.11) (PHOSPHATIDYLINOSITOL SYNTHASE) (PTDINS SYNTHASE) (PI SYNTHASE).//
 10 4.60E-50// 118aa// 86%// O14735
 THYMU3000269// SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT,
 MITOCHONDRIAL PRECURSOR (EC 1.3.5.1) (FP) (FLAVOPROTEIN SUBUNIT OF COMPLEX
 II).// 2.80E-130// 245aa// 99%// P31040
 THYMU3000360
 15 THYMU3001428
 TKIDN2008778
 TKIDN2012771// DPY-19 PROTEIN.// 5.30E-49// 314aa// 35%// P34413
 TKIDN2018926
 TLIVE2001684// complement component 3 precursor [Homo sapiens]// 5.00E-59//
 20 110aa// 32%// NP_000055
 TLIVE2002046// DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24)
 (PORPHOBILINOGEN SYNTHASE) (ALADH).// 3.10E-156// 317aa// 93%// P13716
 TLIVE2007607// CYTOCHROME P450 4A4 (EC 1.14.14.1) (CYP1A4) (PROSTAGLANDIN
 OMEGA- HYDROXYLASE) (P450-P-2).// 6.90E-127// 448aa// 49%// P10611
 25 TRACH1000212
 TRACH2000862// Mus musculus putative purine nucleotide binding protein mRNA,
 complete cds.// 5.40E-224// 619aa// 68%// U44731
 TRACH2007483// GASTRULA ZINC FINGER PROTEIN XLCGF7.1 (FRAGMENT).// 6.30E-12//
 98aa// 37%// P18735
 30 TRACH2019672// Rattus norvegicus mRNA for 45 kDa secretory protein,
 partial.// 5.80E-163// 303aa// 96%// AJ132352
 TRACH2024408// ankyrin 2, isoform 2; ankyrin-2, nonerythrocytic; ankyrin-B;
 ankyrin, brain; ankyrin, neuronal; ankyrin, nonerythroid [Homo sapiens]//
 1.00E-06// 119aa// 20%// NM_020977
 35 TRACH2024559// Homo sapiens myosin 5c (MYO5C) mRNA, complete cds.// 1.70E-
 59// 151aa// 86%// AF272390

- TRACH3000134// ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).// 2.30E-215// 733aa// 53%// P51523
- TRACH3000420// Homo sapiens ATP-binding cassette transporter family A member 12 (ABCA12) mRNA, complete cds.// 7.00E-253// 745aa// 41%// AY033486
- 5 TRACH3002561// UNR protein.// 2.00E-34// 66aa// 95%// P18395
- TRACH3003683// Lactoperoxidase precursor (EC 1.11.1.7) (LP0) (Salivary peroxidase) (SPO).// 1.00E-39// 77aa// 86%// P22079
- TRACH3003832// PHD finger protein 2 [Mus musculus]// 1.00E-153// 321aa// 39%// NM_011078
- 10 TRACH3007866// dipeptidyl peptidase 8; hypothetical protein FLJ20283 [Homo sapiens]// 1.00E-105// 172aa// 53%// NM_017743
- TUTER2000057// Mus musculus AE-1 binding protein AEBP2 mRNA, complete cds.// 1.10E-26// 60aa// 93%// AF090326
- UTERU2004299
- 15 UTERU2008040// Mus musculus mRNA for stac, complete cds.// 3.30E-82// 405aa// 47%// D86639
- UTERU2011220
- UTERU2019534// Golgi apparatus protein 1 [Homo sapiens]// 5.10E-61// 118aa// 100%// XP_012515
- 20 UTERU2021820// dipeptidylpeptidase VI [Homo sapiens]// 8.00E-23// 50aa// 89%// NP_001927
- UTERU2028734// Mus musculus slp2-a mRNA for synaptotagmin-like protein 2-a delta 2S-III, complete cds.// 2.30E-216// 464aa// 86%// AB057762
- UTERU2032279// 47 KDA HEAT SHOCK PROTEIN PRECURSOR (COLLAGEN-BINDING PROTEIN 1) (COLLIGIN 1).// 6.90E-95// 207aa// 93%// P29043
- 25 UTERU2033577// Homo sapiens mRNA for repressor protein, partial cds.// 1.80E-65// 209aa// 65%// D30612
- UTERU2035978
- UTERU3000402
- 30 UTERU3000738// Beta-adrenergic receptor kinase 1 (EC 2.7.1.126) (Beta-ARK-1) (G- protein coupled receptor kinase 2).// 5.00E-76// 139aa// 94%// P26817
- UTERU3001053// zinc finger protein [Homo sapiens]// 0// 319aa// 91%// NM_018651
- UTERU3014791
- 35 UTERU3015069
- UTERU3015412

UTERU3017176

TESTI4038779// zinc finger protein RIN ZF [Rattus norvegicus]// 3.00E-73//

190aa// 36%// NM_024489